

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 111.53 Seconds
(without alignments)
207.149 Million cell updates/sec

Title: US-09-604-325A-46

Perfect score: 1061
Sequence: 1 MKRTYWTITCTIYLQLLPN.....AASSLRNDSSSSSKYIYL 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq 032802:*

- 1: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1980.DAT:*
- 2: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1983.DAT:*
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- 8: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1987.DAT:*
- 9: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1988.DAT:*
- 10: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1989.DAT:*
- 11: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1990.DAT:*
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- 13: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1992.DAT:*
- 14: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1993.DAT:*
- 15: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1994.DAT:*
- 16: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1995.DAT:*
- 17: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1996.DAT:*
- 18: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1997.DAT:*
- 19: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1998.DAT:*
- 20: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA1999.DAT:*
- 21: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/hold-geneSeq/geneSeq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1061	100.0	208	16 AAR83977	Human stem cell fa
2	1061	100.0	208	17 AAR95175	Stem cell factor.
3	1061	100.0	208	21 AAV53286	Human stem cell fa
4	1061	100.0	208	22 AAV05255	Human stem cell fa
5	1061	100.0	208	22 AAB98355	Human stem cell fa
6	1061	100.0	208	22 AAV02457	Human SCF (stem ce
7	1061	100.0	208	22 AAV02457	Human SCF (stem ce
8	1061	100.0	208	22 AAB73565	Human SCF (stem ce
9	1061	100.0	208	22 AAB96940	Human stem cell fa
10	1052	99.2	208	12 AAR11710	Human Stem Cell fa
11	1030	97.1	273	12 AAR11711	Human Stem Cell fa

12	1030	97.1	273	13 AAR20647	Human mast cell gr
13	1030	97.1	273	16 AAR83978	Human stem cell fa
14	1030	97.1	273	18 AAW27607	Human recombinant
15	1030	97.1	273	21 AAV53284	Human SCF protein
16	1030	97.1	273	22 AAV05256	Human SCF protein
17	1030	97.1	273	22 AAV05266	Human SCF protein
18	1030	97.1	273	22 AAB98356	Human stem cell fa
19	1030	97.1	273	22 AAB98357	Human SCF protein
20	1030	97.1	273	22 AAB98357	Human SCF protein
21	1030	97.1	273	22 AAV02458	Human SCF protein
22	1030	97.1	273	22 AAV02460	Human SCF protein
23	1030	97.1	273	22 AAV02765	Human SCF (stem ce
24	1030	97.1	273	22 AAV02766	Human SCF protein
25	1030	97.1	273	22 AAB73566	Human SCF (stem ce
26	1030	97.1	273	22 AAB73567	Human SCF protein
27	1030	97.1	273	22 AAB96941	Human stem cell fa
28	1030	97.1	273	22 AAB96942	Human stem cell fa
29	1030	97.1	273	22 AAB96952	Human stem cell fa
30	1026	96.7	273	22 AAV05257	Monkey SCF protein
31	1026	96.7	273	22 AAB98358	Monkey SCF (stem c
32	1026	96.7	273	22 AAV02484	Monkey SCF protein
33	1026	96.7	273	22 AAV02770	Monkey SCF (stem c
34	1026	96.7	273	22 AAB73571	Monkey SCF (stem c
35	1026	96.7	273	22 AAB96943	Monkey SCF (stem c
36	1021	96.2	273	14 AAR32166	Monkey SCF (stem c
37	1001	94.3	196	22 AAV02456	Human SCF (stem ce
38	1001	94.3	196	22 AAV02763	Human SCF (stem ce
39	1001	94.3	196	22 AAB73564	Human SCF (stem ce
40	1001	94.3	196	22 AAB96939	Human stem cell fa
41	975	91.9	424	16 AAW14765	Human soluble kit
42	974	91.8	424	16 AAW14764	Human soluble kit
43	920	86.7	266	22 AAV05263	Stem cell factor (
44	920	86.7	266	22 AAB98365	Consensus SCF prot
45	920	86.7	266	22 AAV02490	SCF (stem cell fac

ALIGNMENTS

RESULT 1

AA83977 standard; Protein: 208 AA.

AA83977:

14-MAY-1996 (first entry)

Human stem cell factor (SCF).

Stem cell factor; progenitor; haematopoiesis; SCF; anaemia; thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft; transplant; neoplasia; myelosuppression; bone marrow.

Homo sapiens.

Key

Peptide

Protein

Location/Qualifiers

1..25

/label= sig_peptide

26..183

/label= mat_peptide

EP676470-A1.

11-OCT-1995.

04-OCT-1990;

01-OCT-1990;

16-OCT-1989;

11-JUN-1990;

24-AUG-1990;

28-SEP-1990;

90EP-0105391.

90US-0589701.

89US-0422383.

90US-0537198.

90US-0573616.

90WO-US05548.

(AMGE-) AMGEN INC.
 PI Bosselman RA, Martin FH, Suggs SV, Zsebo KM.
 XX
 DR WPI: 1995-346090/45.
 XX N-PSDB; AAT04889.
 XX
 PT New stem cell factor polypeptide(s) - for stimulating the growth of
 PT primitive progenitor cells, esp. for treating disorders involving
 XX blood cells
 XX
 PS Disclosure: Fig 15C; 127pp; English.
 XX
 CC AAR83997 is human stem cell factor (SCF). Non-naturally occurring SCF
 CC and C-terminally truncated polypeptides stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem cells
 CC and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia, for
 CC enhancing engraftment of bone marrow during transplantation or for
 CC bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for the
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 CC
 SQ Sequence 208 AA;
 XX
 Query Match 100.0%; Score 1061; DB 16; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCIYQLLEFNPLVTEGICRNRYNNVKDVTKIVANLPKQWITLKYPG 60
 DB 1 mktqtwiltciyqllefnplvtegeicrnyvnnvkdvtklvanlpkqwmiltkyypg 60
 QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVCEKENS 120
 DB 61 mdvlpshcwissemvqvsldtdldkfsnlsesglnsyisldklvinivdvlvecvknss 120
 QY 121 KDLSKFSPEPRLTPEEFPRIRNRSIDAFKDFVASETSDCVVSTLSPEKDSRVSVT 180
 DB 121 kdlskfskpspeprltpeefirifnrsidafkdfvasetsdcvvsstlspekdsrvsvt 180
 QY 181 KPFMLPVAASSLRNDSSSNSKRYIYL 208
 DB 181 kpfmlppvaasslrndssnskskryiyl 208
 RESULT 2
 AAR95175 standard; Protein; 208 AA.
 XX
 AC AAR95175;
 XX
 DT 03-OCT-1996 (first entry)
 XX
 DE Stem cell factor.
 XX
 KW Stem cell factor: SCF; splice variant; embryo implantation;
 KM in vitro fertilisation; IVF.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..25 Location/Qualifiers
 FT Protein /label= Sig.peptide
 FT 26..208
 FT /label= Mat.protein
 XX

PN W09614410-A1.
 XX
 PD 17-MAY-1996.
 XX
 PF 31-OCT-1995; 95WO-GB02547.
 XX
 PR 28-APR-1995; 95GB-0008618.
 XX 04-NOV-1994; 94GB-0022293.
 XX
 PA (ISTE) ARS APPLIED RES SYST HOLDING NV.
 XX
 PI Dellow KA, Sharkey AM, Smith SK;
 XX
 DR WPI: 1996-251760/25.
 XX N-PSDB; AAT29489.
 XX
 PT Stem cell factor comprising C-terminal sequence given in
 PT specification - useful to ensure correct development of
 PT pre-implantation embryos before implantation into subject
 XX
 PS Disclosure: Fig 2; 25pp; English.
 XX
 CC A DNA sequence (AAT29489) codes for human stem cell factor (SCF)
 CC (AAR95175). The full-length SCF transcript consists of 8 exons.
 CC A novel splice variant has been identified that appears to arise
 CC from the inclusion of a novel exon (see also AAT29488) between exons
 CC 3 and 4 of the gene. The resulting frameshift produces a novel
 CC SCF consisting of the first 39 amino acids of mature SCF followed
 CC by a 33-amino acid C-terminal region (AAR95174). The novel SCF is
 CC useful for ensuring correct development of pre-implantation embryos.
 CC
 SQ Sequence 208 AA;
 XX
 Query Match 100.0%; Score 1061; DB 17; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCIYQLLEFNPLVTEGICRNRYNNVKDVTKIVANLPKQWITLKYPG 60
 DB 1 mktqtwiltciyqllefnplvtegeicrnyvnnvkdvtklvanlpkqwmiltkyypg 60
 QY 61 MDVLPSCWISSEMVQVLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVCEKENS 120
 DB 61 mdvlpshcwissemvqvsldtdldkfsnlsesglnsyisldklvinivdvlvecvknss 120
 QY 121 KDLSKFSPEPRLTPEEFPRIRNRSIDAFKDFVASETSDCVVSTLSPEKDSRVSVT 180
 DB 121 kdlskfskpspeprltpeefirifnrsidafkdfvasetsdcvvsstlspekdsrvsvt 180
 QY 181 KPFMLPVAASSLRNDSSSNSKRYIYL 208
 DB 181 kpfmlppvaasslrndssnskskryiyl 208
 RESULT 3
 AAY53286 standard; Protein; 208 AA.
 XX
 AC AAY53286;
 XX
 DT 27-JUL-2000 (first entry)
 XX
 DE Human stem cell factor protein sequence.
 XX
 KW Stem cell factor: SCF; haematopoietic progenitor cell; blood forming;
 KM primitive progenitor cell; haematopoietic disorder; syngeneic;
 KM allogeneic; autologous bone marrow transplant; gene therapy;
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
 XX cancer.
 XX
 OS Homo sapiens.
 XX

PN EP992579-A1.
 XX 12-APR-2000.
 PD
 XX 04-OCT-1990; 99EP-0122861.
 PF
 XX 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90MO-US05548.
 PR 01-OCT-1990; 90US-0589701.
 PR 04-OCT-1990; 90EP-0310899.
 XX
 PA (AMGE-) AMGEN INC.
 PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH.
 XX
 DR WPI: 2000-259135/23.
 DR N-PSDB; AAM13716.
 XX
 PT Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -
 XX
 PS Claim 21; Fig 15C; 123pp; English.
 XX
 CC A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining
 CC hematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting
 CC hematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC hematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a specifically claimed human SCF from the present invention.
 CC
 XX
 SQ Sequence 208 AA;

Query Match 100.0%; Score 1061; DB 21; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILLCIYIQLLEFNPLVKTGICRNRYNNVKNVAVLPRKDYMITLKYVPG 60
 DB 1 MKKTQWILLCIYIQLLEFNPLVKTGICRNRYNNVKNVAVLPRKDYMITLKYVPG 60
 QY 61 MDVLPSCWISSEWVOLSLSLFDLDFKSNISGLSNYSIIDKLXNIVDLEVCVENSS 120
 DB 61 MDVLPSCWISSEWVOLSLSLFDLDFKSNISGLSNYSIIDKLXNIVDLEVCVENSS 120
 QY 121 KDLKSKSPSEPRUFTPEEFRRFNRSIDAFKPFVVAASESDCVVSTISPEKDSRVST 180
 DB 121 KDLKSKSPSEPRUFTPEEFRRFNRSIDAFKPFVVAASESDCVVSTISPEKDSRVST 180
 QY 181 KPFMLPVAASSLRNDSSSSNSKYIYLI 208
 DB 181 KPFMLPVAASSLRNDSSSSNSKYIYLI 208

RESULT 4
 AAU05255

ID AAU05255 standard; Protein; 208 AA.
 XX
 AC AAU05255;
 XX
 DT 24-OCT-2001 (first entry)
 DT
 XX
 DE Human stem cell factor (SCF) protein encoded by SCF cDNA.
 XX
 KW Human; stem cell factor; SCF; hematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= signal_peptide
 FT 26..208
 FT Protein /label= Mature_SCF
 XX
 FN US6248319-B1.
 XX
 PD 19-JUN-2001.
 XX
 PE 24-MAY-1995; 95US-0449653.
 XX
 PR 10-APR-1991; 91US-0684535.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR 21-DEC-1993; 93US-0172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselmann RA, Suggs SV, Martin FH;
 XX
 DR WPI: 2001-407312/43.
 DR N-PSDB; AAM10457.
 XX
 PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 PS
 XX
 SQ Example 3; Fig 15C; 210pp; English.
 CC The present sequence represents human stem cell factor (SCF). The
 CC sequence is described in an invention relating to novel stem cell
 CC factors, the polynucleotides encoding them and methods for producing
 CC the stem cell factors. The methods involve increasing the number of
 CC early haematopoietic progenitor cells in human peripheral blood by
 CC administering a haematopoietically effective human stem cell factor
 CC polypeptide. The methods are useful for the treatment of blood
 CC disorders, including myelofibrosis, myelocytosis, osteopetrosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folic acid deficiency,
 CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
 CC including AIDS.
 CC
 XX
 SQ Sequence 208 AA;

Query Match 100.0%; Score 1061; DB 22; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILLCIYIQLLEFNPLVKTGICRNRYNNVKNVAVLPRKDYMITLKYVPG 60

```

Db      1 mktqtwlilcylqlllfnplvktegicrnrvnmvkdvtkivanlpxkymtlkypg 60
QY      61 MDVLPSCWISSEWVVOVSDSLFDLDFKFSNISSEGLSNYSIIDKLVIIVDVLVECVKENS 120
Db      61 mdvlpschwissemvvglsdldldkfnsiseglsnysiidklvniivddlvecvken 120
QY      121 KDLKSKFSPEPRFLFPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db      121 kdllksfkspetrlfpeefrfrinsidafkdfvaasetdcvssltlspkdsrvsvt 180
QY      181 KPFLMPVAAASLRNDSSSSNSKYIYLI 208
Db      181 kpflmpvaasslrndssssnskyiyl 208

RESULT 5
ID      AAB98355 standard; Protein; 208 AA.
AC      AAB98355;
XX
XX      21-AUG-2001 (first entry)
DT
DE      Human stem cell factor (SCF) protein SMO ID NO:46.
KW      Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW      gene therapy.
OS      Homo sapiens.
XX
XX      US6207454-B1.
PN
PD      27-MAR-2001.
XX
XX      31-DEC-1998; 98US-0224681.
PE
XX      21-DEC-1993; 93US-0172329.
PR      24-MAY-1995; 95US-0449653.
PR      12-JAN-1998; 98US-0005893.
PR      25-NOV-1992; 92US-0982255.
PR      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      01-OCT-1990; 90US-0589701.
XX
XX      (AMGE-) AMGEN INC.
PA
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI
XX      WPI: 2001-366062/38.
DR      N-PSDB; AAH41341.
XX
XX      Enhancing efficiency of transfer of polynucleotide into a target
PT      mammalian cell in vitro, involves exposing cell that expresses a stem
PT      cell factor receptor to stem cell factor, and introducing
PT      polynucleotide into cell in vitro -
XX
XX      Claim 16; Fig 15C; 210pp; English.
XX
XX      The present invention describes a method for enhancing (E) the
CC      efficiency of transfer of a polynucleotide (I) into a target mammalian
CC      cell (II) in vitro, comprising exposing (II) that expresses a stem cell
CC      factor (SCF) receptor to a biologically active SCF, its analogue or
CC      fragment, which induces cell proliferation, and introducing (I) to (II)
CC      in vitro. Exposure of SCF to (II) results in increased uptake of (I)
CC      into the cell. The method is useful for enhancing the efficiency of the
CC      transfer of a polynucleotide into a target mammalian cell in vitro.
CC      The method is useful in gene therapy techniques. AAH41301 to AAH41364
CC      and AAB98351 to AAB98390 represent sequences used in the exemplification
CC      of the present invention.
XX
XX      Sequence 208 AA;
SQ

```

```

Query Match      100.0%; Score 1061; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 3,8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKKTQWILTCIYQLLLFNPLVTEGICRNRYNNKDYTKIVANLPRXYMTITIKYVP 60
Db      1 mktqtwlilcylqlllfnplvktegicrnrvnmvkdvtkivanlpxkymtlkypg 60
QY      61 MDVLPSCWISSEWVVOVSDSLFDLDFKFSNISSEGLSNYSIIDKLVIIVDVLVECVKENS 120
Db      61 mdvlpschwissemvvglsdldldkfnsiseglsnysiidklvniivddlvecvken 120
QY      121 KDLKSKFSPEPRFLFPEEFRIENRSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db      121 kdllksfkspetrlfpeefrfrinsidafkdfvaasetdcvssltlspkdsrvsvt 180
QY      181 KPFLMPVAAASLRNDSSSSNSKYIYLI 208
Db      181 kpflmpvaasslrndssssnskyiyl 208

RESULT 6
ID      AAU02457 standard; Protein; 208 AA.
AC      AAU02457;
XX
XX      29-AUG-2001 (first entry)
DT
DE      Human SCF (stem cell factor) protein encoded by SCF cDNA.
XX
XX      Human: stem cell factor; SCF; early haematopoietic progenitor cell;
KW      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW      anaemia; kala azar; septicemia; malaria; hypopigmentation disorder.
XX
XX      Homo sapiens.
OS
XX
XX      Key Location/Qualifiers
FH      Peptide 1..25
FT      /label= Signal_peptide
FT      Protein 26..208
FT      /label= Mature_SCF
XX
XX      US6207417-B1.
PN
XX
XX      27-MAR-2001.
PD
XX
XX      07-JUN-1995; 95US-0482918.
PE
XX      21-DEC-1993; 93US-0172329.
PR      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      01-OCT-1990; 90US-0589701.
XX
XX      (ZSEB/) ZSEBO K M.
PA      (BOSS/) BOSSELMAN R A.
PA      (SUGG/) SUGGS S V.
PA      (MART/) MARTIN F H.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI
XX      WPI: 2001-298941/31.
DR      N-PSDB; AAS04121.
XX
XX      Novel nucleic acids encoding stem cell factor useful for treating
PT      disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
PT      disease, kala azar, anaemia and septicemia -
XX
XX      Example 3; Fig 15C; 209pp; English.
XX

```


CC The present sequence represents human SCF (stem cell factor) protein
 CC encoded by SCF cDNA. The present invention relates to novel stem cell
 CC factors (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides
 CC encoding them. SCF stimulate primitive progenitor cells including early
 CC haematopoietic progenitor cells. The invention also describes SCF
 CC peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.

CC Sequence 208 AA:

Query Match 100.0%; Score 1061; DB 22; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTTKYVG 60
 DB 1 mkkqtwtlctiyqlllfnplvktegicrnrvtnnvdklvankpdymltkyvgp 60
 QY 61 MDVLPSCWISSEMYVQSDSLTDLDFKFSNISEGLSNTSIIDKLVNIYVDLVECKENSS 120
 DB 61 mdvlpshcwisemvqdsldtldkfsniseqlsnytsidklniivddlveckenss 120
 QY 121 KDLKSKFSPEPRILFPEEFRIFNRSIDAFKDFVVASETSCVVSSTLSPKDSRVSVT 180
 DB 121 kdlksfkspeprilfpeeffriinrsidafkdfvvasetscvvstlspekdsrvsvt 180
 QY 181 KPFLMPVAASSLRNDSSSSNSKRYIYL 208
 DB 181 kpflmpvaasslrndssssnskryiyl 208

RESULT 7

ID AAU02764 standard; Protein: 208 AA.

AC AAU02764;

XX 29-AUG-2001 (first entry)

DE Human SCF (stem cell factor) protein encoded by SCF cDNA.

KM Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KM blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KM anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /Label= Signal_peptide

FT /Label= Mature_SCF

PN US6218148-B1.

PD 17-APR-2001.

PF 21-DEC-1993;

XX 25-NOV-1992;

PR 16-OCT-1989;

PR 11-JUN-1990;

PR 24-AUG-1990;

PR 01-OCT-1990; 90US-0589701.

XX (AMGE-) AMGEN INC.

PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;

DR WPI: 2001-281051/29.

DR N-PSDB; AAS04222.

XX

PS Example 3; Fig 15C; 167pp; English.

CC The present sequence represents human SCF (stem cell factor) protein
 CC encoded by SCF cDNA. The present invention relates to novel stem cell
 CC factors (AAU02761-AAU02765, AAU02770-AAU02775, AAU02797) and the
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04218) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.

XX Sequence 208 AA:

Query Match 100.0%; Score 1061; DB 22; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.8e-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRVTNNVQVTKLVANLPKDYMTTKYVG 60
 DB 1 mkkqtwtlctiyqlllfnplvktegicrnrvtnnvdklvankpdymltkyvgp 60
 QY 61 MDVLPSCWISSEMYVQSDSLTDLDFKFSNISEGLSNTSIIDKLVNIYVDLVECKENSS 120
 DB 61 mdvlpshcwisemvqdsldtldkfsniseqlsnytsidklniivddlveckenss 120
 QY 121 KDLKSKFSPEPRILFPEEFRIFNRSIDAFKDFVVASETSDCVVSSTLSPKDSRVSVT 180
 DB 121 kdlksfkspeprilfpeeffriinrsidafkdfvvasetscvvstlspekdsrvsvt 180
 QY 181 KPFLMPVAASSLRNDSSSSNSKRYIYL 208
 DB 181 kpflmpvaasslrndssssnskryiyl 208

RESULT 8

ID AAB73565 standard; Protein: 208 AA.

AC AAB73565;

XX 07-AUG-2001 (first entry)

DE Human SCF (stem cell factor) protein #2, encoded by SCF cDNA.

KM Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KM blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KM anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.

OS Homo sapiens.

XX

XX Key

FT Peptide

FT

```

FT      /label= signal_peptide
FT      26..208
FT      Protein
FT      /label= Mature_SCF
XX
XX      US6204363-B1.
XX
XX      20-MAR-2001.
XX
XX      25-NOV-1992; 92US-0982255.
XX
XX      10-APR-1991; 91US-0684535.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX
XX      (AMGE-) AMGEN INC.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX      WPI: 2001-256683/26.
XX      N-PSDB; AAH23899.
XX
XX      New stem cell factor polypeptides and their analogs which stimulate
XX      growth of early hematopoietic progenitors, useful for treating aplastic
XX      anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX      disease
XX
XX      Claim 1; Fig 15C; 166pp; English.
XX
XX      The present sequence represents human SCF (stem cell factor) protein
XX      encoded by SCF cDNA. The present invention relates to novel stem cell
XX      factors (AAH23561-AAH23568, AAH23571-AAH23576) and the
XX      polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX      including early haematopoietic progenitor cells. The invention also
XX      describes SCF peptides (AAH23578-AAH23597) and the oligonucleotides
XX      (AAH23859-AAH23895) used in the isolation of human and rat SCF
XX      sequences. The polynucleotide encoding SCF is useful for producing
XX      SCF and useful in gene therapy. It is useful for treating disorders
XX      involving blood cells such as myelofibrosis, metastatic carcinoma,
XX      acute leukemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX      Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
XX      sarcoidosis, military tuberculosis, disseminated fungus disease,
XX      fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX      pyridoxine deficiency, and hypopigmentation disorders such as
XX      piebaldism and vitiligo.
XX
XX      Sequence 208 AA:
SQ

```

```

ID      AAB96940 standard; Protein; 208 AA.
XX
XX      AAB96940;
XX
XX      13-JUL-2001 (first entry)
XX
XX      Human stem cell factor SEQ ID NO: 46.
XX
XX      Human: rat; mammal; stem cell factor; SCF; cell growth stimulation;
XX      gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
XX      neurological damage; intestinal damage; infertility; AIDS; SCID;
XX      severe combined immunodeficiency.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Peptide 1..25
XX      Protein /label= signal_peptide
XX      /label= mature_stem_cell_factor
XX
XX      US6207802-B1.
XX
XX      27-MAR-2001.
XX
XX      09-NOV-1994; 94US-0336728.
XX
XX      25-NOV-1992; 92US-0982255.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX
XX      (AMGE-) AMGEN INC.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX      WPI: 2001-353108/37.
XX      N-PSDB; AAF89101.
XX
XX      Novel isolated non-human mammalian stem cell factor polypeptide
XX      stimulating growth of early haematopoietic progenitor cells, useful for
XX      treating aplastic anaemia, lymphoma, Letterer-Siwe disease, kala azar,
XX      sarcoidosis -
XX
XX      Disclosure; Fig 15C; 209pp; English.
XX
XX      The present invention provides the protein and coding sequences of
XX      mammalian stem cell factors (SCFs). These are capable of stimulating the
XX      growth of early haematopoietic progenitor cells, neural stem cells and
XX      primordial germ stem cells. The sequences are useful in the treatment of
XX      leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
XX      nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX      and intestinal damage, infertility, AIDS and severe combined
XX      immunodeficiency (SCID). The present sequence is an SCF described in the
XX      invention.
XX
XX      Sequence 208 AA:
SQ

```

```

Query Match      100.0%; Score 1061; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match      100.0%; Score 1061; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.8e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

DB 121 KDLKSKFSKSPRILFTPEEFIRLFRSIDAFKDFVAVASLSDCVVSTLSPEKDSRVSVT 180
 QY 181 KPFLPPEVAASLRNDSSSSSKYIYL 208
 DB 181 KPFLPPEVAASLRNDSSSSSKYIYL 208

RESULT 10

AA011710
 ID AAR11710 standard; Protein: 208 AA.

AC AAR11710;

DT 20-JUN-1991 (first entry)

DE Human Stem Cell Factor.

KW Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /label= sig_peptide

FT Protein 26..208 /label= mat_protein

EP423980-A.

PD 24-APR-1991.

PF 04-OCT-1990; 90EP-0310899.

PR 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-0505548.

PA (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;

DR WPI: 1991-119233/17.

DR N-PSDB; AAQ11540, AAQ11541.

XX New naturally-occurring polypeptide stem cell factor analogues -

PT have haematopoietic biological activity of stem cell factor and

PT are used to treat eg leukopenia, AIDS, nerve damage and

PT infertility

PS Disclosure; Fig 15C; 127pp; English.

XX The SCF has the ability to stimulate growth of primitive

CC progenitors including early hematopoietic progenitor cells and non-

CC hematopoietic stem cells such as neural stem cells and primordial

CC germ stem cells. The product may be used in a pharmaceutical

CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,

CC anaemia, AIDS, neoplasia, nerve damage, infertility and

CC intestinal damage.

CC See also AAR11708, AAQ11509-Q11543.

XX Sequence 208 AA;

SO

Query Match

Best local Similarity 99.2%; Score 1052; DB 12;

Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWIIITCIYLLQLLEPLVKEGICRNRVTNNVKVATLVANLPDYMITLKYVPG 60

DB 1 MKKTQWIIITCIYLLQLLEPLVKEGICRNRVTNNVKVATLVANLPDYMITLKYVPG 60

QY 61 MDVLPSCHWISEWVOLSRLDLDKFSNISGSLNYSIIDKLVNIYDDLYECKENSS 120
 DB 61 MDVLPSCHWISEWVOLSRLDLDKFSNISGSLNYSIIDKLVNIYDDLYECKENSS 120
 QY 121 KDLKSKFSKSPRILFTPEEFIRLFRSIDAFKDFVAVASLSDCVVSTLSPEKDSRVSVT 180
 DB 121 KDLKSKFSKSPRILFTPEEFIRLFRSIDAFKDFVAVASLSDCVVSTLSPEKDSRVSVT 180
 QY 181 KPFLPPEVAASLRNDSSSSSKYIYL 208
 DB 181 KPFLPPEVAASLRNDSSSSSKYIYL 208

RESULT 11

AA011711
 ID AAR11711 standard; Protein: 273 AA.

AC AAR11711;

DT 20-JUN-1991 (first entry)

DE Human Stem Cell Factor from HT1080 fibrosarcoma line.

KW Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25 /label= sig_peptide

FT Protein 26..273 /label= mat_protein

EP423980-A.

PD 24-APR-1991.

PF 04-OCT-1990; 90EP-0310899.

PR 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-0505548.

PA (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;

DR WPI: 1991-119233/17.

DR N-PSDB; AAQ11542.

XX New naturally-occurring polypeptide stem cell factor analogues -

PT have haematopoietic biological activity of stem cell factor and

PT are used to treat eg leukopenia, AIDS, nerve damage and

PT infertility

PS Disclosure; Fig 42; 127pp; English.

XX The SCF has the ability to stimulate growth of primitive

CC progenitors including early hematopoietic progenitor cells and non-

CC hematopoietic stem cells such as neural stem cells and primordial

CC germ stem cells. The product may be used in a pharmaceutical

CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,

CC anaemia, AIDS, neoplasia, nerve damage, infertility and

CC intestinal damage.

CC See also AAR11708, AAQ11509-Q11543.

XX Sequence 273 AA;

SO

Query Match

Best local Similarity 97.1%; Score 1030; DB 12; Length 273;

Best Local Similarity 99.5%; Pred. No. 1,1e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKKTQWIIITCIYQLLEPNPLVKTEGICRNRYNNVADYKLVANLPKDYITLKYPG 60
DB 1 mkkctwiltciylqllfnplvktegicrnrvtnvkvtklvankpdyimltikypg 60
OY 61 MDVPSHCWISEMNVQSLDLSITDLDFNSISEGLSNYSIIDKLVINIYVDLVECKENSS 120
DB 61 mdvlpshcwisemvqvqlsdltdlkdksnlsesglsnysiidklvniyvdllveckenss 120
OY 121 KDLKSFSPERLFTPEEFRRIFNKSIDAKDFVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 kdllksfkspeprlftpeeffrrifnksidafkdfvasetsdcvvsstlspekdsrvsvt 180
OY 181 KPEMLPVAASSLRNDSSSNSK 203
DB 181 kpfmlpvaasslrndsssnrk 203

RESULT 12

AAR20647
ID AAR20647 standard; Protein: 273 AA.

AC AAR20647;

DT 30-APR-1992 (first entry)

DE Human mast cell growth factor.

KW hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
proliferation.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= signal
FT Region 26..210
FT /label= extracellular
FT /note= "claimed polypeptide"
FT Region 211..237
FT /label= transmembrane
FT Region 238..273
FT /label= intracellular

PN WO9200376-A.

PD 09-JAN-1992.

FE 14-JUN-1991; 91WO-US04274.

XX 25-JUN-1990; 90US-0543264.

PR 10-AUG-1990; 90US-0565840.

PR 28-AUG-1990; 90US-0574152.

PR 21-SEP-1990; 90US-0586073.

PR 12-JUN-1991; 91US-0713715.

PA (IMMO-) IMMUNEX CORP.

XX Williams DE, Lyman S;

PI WPI; 1992-041558/05.

DR N-PSDB; AAQ20845.

XX New isolated DNA encoding human mast cell growth factor - useful in
PT stimulating proliferation of hematopoietic cells with growth factor,
PT to treat haemolytic and hypoproliferative anaemias
XX Claim 10; Fig 4; 59pp; English.
PS This human MGF has a mature extracellular region of 185 amino acids.
CC There is a second form of hMGF (see AAQ20844) resulting from an

CC alternative mRNA splicing event which deletes an exon encoding an
CC additional 28 amino acids beginning at amino acid 148 of the mature
CC protein. MGF is the ligand for the protein receptor expression product
CC of the c-kit proto-oncogene. MGF can be used to augment the
CC activity of other cytokines. It can influence early lymphoid or
CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
XX
SQ Sequence 273 AA:

Query Match 97.1%; Score 1030; DB 13; Length 273;
Best Local Similarity 99.5%; Pred. No. 1,1e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKKTQWIIITCIYQLLEPNPLVKTEGICRNRYNNVADYKLVANLPKDYITLKYPG 60
DB 1 mkkctwiltciylqllfnplvktegicrnrvtnvkvtklvankpdyimltikypg 60
OY 61 MDVPSHCWISEMNVQSLDLSITDLDFNSISEGLSNYSIIDKLVINIYVDLVECKENSS 120
DB 61 mdvlpshcwisemvqvqlsdltdlkdksnlsesglsnysiidklvniyvdllveckenss 120
OY 121 KDLKSFSPERLFTPEEFRRIFNKSIDAKDFVASETSDCVVSTLSPEKDSRVSVT 180
DB 121 kdllksfkspeprlftpeeffrrifnksidafkdfvasetsdcvvsstlspekdsrvsvt 180
OY 181 KPEMLPVAASSLRNDSSSNSK 203
DB 181 kpfmlpvaasslrndsssnrk 203

RESULT 13

AAR83978
ID AAR83978 standard; Protein: 273 AA.

AC AAR83978;

DT 15-MAY-1996 (first entry)

DE Human stem cell factor derived from HT1080 fibrosarcoma cell line.

KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
transplant; neoplasia; myelosuppression; bone marrow; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= sig_peptide
FT Protein 26..248
FT /label= mat_SCF

PN EP676470-A1.

PD 11-OCT-1995.

FE 04-OCT-1990; 90EP-0105391.

XX 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-US05548.

PA (AMGE-) AMGEN INC.

XX Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
PI WPI; 1995-346090/45.
DR N-PSDB; AAT04890.
XX New stem cell factor polypeptide(s) - for stimulating the growth of

PT primitive progenitor cells, esp. for treating disorders involving blood cells

PS Claim 9; Fig 42; 127pp; English.

XX AAR83978 is a human stem cell factor (SCF) derived from the HT1080 fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally occurring SCF, stimulate growth of primitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertility, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7.

CC Sequence 273 AA;

SQ

Query Match 97.1%; Score 1030; DB 16; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCYIQLLEPLNPLVKTGICRNRVNNVADVKLVANLPKDMITLKYPG 60
DB 1 mktqtwtlctyqlllfplnvktgicrnrvnnvdklvannlpkdymltkypg 60

QY 61 MDVLPSCWISSEMVVQLSDSLTDLKPSNISEGNSYIIDKLVNIVYDVLVECKENSS 120
DB 61 mdvlpshcwisemvvglsdsltldkpsniseglsnyiidklynvivdvlveckkess 120

QY 121 KDIAKSFSPERLFTPEEFRIENRSIDAFKDVVASSETSDCVVSTLSPKDSRVSVT 180
DB 121 kdiksfkspeprlftpeefrinfnsidafrkdvvasetsdcvvsstlspkdsrvsvt 180

QY 181 KPMPPPVAASLRNDSSSSNSK 203
DB 181 kpmpppvaaslrndssssnsk 203

RESULT 14
AAW27607
ID AAW27607 standard; Protein: 273 AA.
XX AAW27607;
XX AAW27607;
XX 28-APR-1998 (first entry)
XX Human recombinant stem cell factor protein.
XX DE
XX Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
KW SF; analog; treatment; haematopoietic factor; progenitor cell;
XX pigmentation disorder; haematopoietic disorder.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= leader sequence
FT Protein 26..274
FT /note= "mature full length stem cell factor protein"
XX M09738101-A1.
XX 16-OCT-1997.
XX PD
XX 03-APR-1997; 97WO-US05541.

XX 05-APR-1996; 9605-0628428.
XX (AMGE-) AMGEN INC.
XX Lu HS;
XX WPI; 1997-512718/47.
XX Stem cell factor analogue N10D or N10P/N11D - useful to treat
PT pigmentation disorder; AIDS; nerve damage; infertility; intestinal
PT damage or haematopoietic disorder
XX

PS Claim 2; Fig 1; 42pp; English.

XX This sequence represents a membrane bound form of a human recombinant stem cell factor (SCF). Stem cell factors are also known as mast cell growth factors (MCGF) or Steel factors (SF or SLF) are haematopoietic factors which act on haematopoietic progenitor cells. Analogues of a wild type SCF sequence have been constructed (see AAW27605 and AAW27606) which have increased biological activity and stability compared to unmodified SCF and can be used to treat pigmentation disorders, e.g. vitiligo, acquired immunodeficiency syndrome, nerve damage, infertility, intestinal damage or a haematopoietic disorder, e.g. leucopenia, CC thrombocytopenia or anaemia, enhance bone marrow engraftment during CC transplantation or bone marrow recovery following radiation, chemical or chemotherapy, induced bone marrow aplasia or myelosuppression, CC sensitive cells to chemotherapy or mobilise peripheral blood progenitor cells. It can also be used in an in vitro haematopoietic cell, preferably CC bone marrow or peripheral blood progenitor cell, culture medium, where the cells are optionally subsequently transfected with exogenous DNA.

SQ Sequence 273 AA;

Query Match 97.1%; Score 1030; DB 18; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCYIQLLEPLNPLVKTGICRNRVNNVADVKLVANLPKDMITLKYPG 60
DB 1 mktqtwtlctyqlllfplnvktgicrnrvnnvdklvannlpkdymltkypg 60

QY 61 MDVLPSCWISSEMVVQLSDSLTDLKPSNISEGNSYIIDKLVNIVYDVLVECKENSS 120
DB 61 mdvlpshcwisemvvglsdsltldkpsniseglsnyiidklynvivdvlveckkess 120

QY 121 KDIAKSFSPERLFTPEEFRIENRSIDAFKDVVASSETSDCVVSTLSPKDSRVSVT 180
DB 121 kdiksfkspeprlftpeefrinfnsidafrkdvvasetsdcvvsstlspkdsrvsvt 180

QY 181 KPMPPPVAASLRNDSSSSNSK 203
DB 181 kpmpppvaaslrndssssnsk 203

RESULT 15
AAW53284
ID AAW53284 standard; Protein: 273 AA.
XX AAW53284;
XX AAW53284;
XX 27-JUL-2000 (first entry)
XX Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
XX DE
XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW primitive progenitor cell; haematopoietic disorder; syngeneic;
KW allogeneic; autologous bone marrow transplant; gene therapy;
XX transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX cancer.
XX Homo sapiens.
XX OS

Search completed: August 18, 2002, 13:08:01
Job time: 406 sec

XX EP92579-A1.
PN
XX
PD 12-APR-2000.
XX
PF 04-OCT-1990; 99EP-0122861.
XX
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90WO-0505548.
PR 01-OCT-1990; 90US-0589701.
PR 04-OCT-1990; 90EP-0310899.
XX
XX (AMGE-) AMGEN INC.
PA
XX Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
PI
XX
XX WPI: 2000-259135/23.
DR N-PSDB; AAA13714.
XX
XX Production of hematopoietic cells suitable for administration to a
PT subject using progenitor cells and expanding the cells using stem cell
PT factor -
XX
XX
PS Claim 22; Fig 42; 123pp; English.
XX
CC A method has been developed of making haematopoietic cells suitable for
CC administration to a subject. The method comprises: (a) obtaining
CC haematopoietic progenitor cells from a donor; and (b) expanding the
CC cells by adding to the cells a haematopoietically effective dose of a
CC polypeptide product having at least part of the primary structural
CC confirmation and one or more of the biological properties of naturally
CC occurring stem cell factor (SCF). The method is useful for stimulating
CC primitive progenitor cells including early haematopoietic progenitor
CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is
CC useful for expanding early haematopoietic progenitors in syngeneic,
CC allogeneic or autologous bone marrow transplant. SCF is useful for
CC enhancing the efficiency of gene therapy based on transfecting
CC haematopoietic stem cells. SCF is also useful for combating the
CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
CC haematopoietic recovery after acute blood loss and as a boost to the
CC immune system for fighting neoplasia (cancer). The present sequence
CC represents a specifically claimed human SCF from the present invention.
XX
XX
SQ Sequence 273 AA;

Query Match 97.1%; Score 1030; DB 21; Length 273;
Best Local Similarity 99.5%; Pred. No. 1.1e-100;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQMTITCTIYQLLFNPLVTEGICRNRTNNVKDYTKLVANLPKDYMTITLKYVG 60
DB 1 mktgtwtltctlyqlllfnplvktegicrnrvtnnvkdvcklvannlpkdymtitlkyvg 60
QY 61 MDVLPSCWISBMYVQSLDLDLDFKFSNTSEGLSNYSIIDKLNVYVDLVECKENSS 120
DB 61 mdvlpshcwisemvyqslsdldldkfsnlselsglsmysiidklvniyvdldveckenss 120
QY 121 KDIKSEKSPPEPLFTPEEFRIIFNRSIDAKDFVASETSDCVVSSSTLSPKXSRVSVT 180
DB 121 kdlkksksppeplftpeefrifiifnrSIDAKDFVASETSDCVVSSSTLSPKXSRVSVT 180
QY 181 KPFMLPVAASLRNDSSSSNSK 203
DB 181 kpfmlpvaaslrndssssnsk 203

Sun Aug 18 14:09:01 2002

us-09-604-325a-46.rag

Page 11

4
1
1
1
1

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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 41.62 Seconds
(without alignments)
122.069 Million cell updates/sec

Title: US-09-604-325a-46

Perfect score: 1061

Sequence: 1 MKKTQWILTCIYLQLLFN.....AASLRNDSNSSKYYLI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1061	100.0	208	4	US-08-836-252A-6
2	1061	100.0	208	4	US-08-482-918-46
3	1061	100.0	208	4	US-09-224-681-46
4	1061	100.0	208	4	US-08-336-728A-46
5	1030	97.1	273	1	US-08-220-379B-2
6	1030	97.1	273	2	US-08-628-428-9
7	1030	97.1	273	4	US-08-482-918-48
8	1030	97.1	273	4	US-08-482-918-49
9	1030	97.1	273	4	US-08-482-918-61
10	1030	97.1	273	4	US-09-224-681-48
11	1030	97.1	273	4	US-09-224-681-49
12	1030	97.1	273	4	US-09-224-681-61
13	1030	97.1	273	4	US-08-336-728A-48
14	1030	97.1	273	4	US-08-336-728A-49
15	1030	97.1	273	4	US-08-336-728A-61
16	1026	96.7	273	4	US-08-482-918-50
17	1026	96.7	273	4	US-09-224-681-50
18	1026	96.7	273	4	US-08-336-728A-50
19	1001	94.3	196	4	US-08-336-728A-44
20	975	91.9	424	5	PCT-US95-03866-14
21	974	91.8	424	5	PCT-US95-03866-12
22	920	86.7	266	4	US-08-482-918-57
23	920	86.7	266	4	US-09-224-681-57
24	920	86.7	266	4	US-08-336-728A-57
25	898	84.6	248	4	US-08-955-848A-82
26	897.5	84.6	274	4	US-08-336-728A-52
27	896.5	84.5	205	1	US-08-133-979A-4

28	896.5	84.5	205	2	US-08-436-890-4	Sequence 4, Appl
29	896.5	84.5	205	2	US-08-451-213-4	Sequence 4, Appl
30	890	83.9	245	4	US-08-482-918-63	Sequence 63, Appl
31	890	83.9	245	4	US-09-224-681-63	Sequence 63, Appl
32	890	83.9	245	4	US-08-336-728A-63	Sequence 63, Appl
33	884	83.3	271	4	US-08-482-918-52	Sequence 52, Appl
34	884	83.3	271	4	US-09-224-681-52	Sequence 52, Appl
35	880.5	83.0	274	4	US-08-336-728A-53	Sequence 53, Appl
36	875	82.5	273	4	US-08-482-918-53	Sequence 53, Appl
37	875	82.5	273	4	US-09-224-681-53	Sequence 53, Appl
38	865	81.5	195	4	US-08-482-918-44	Sequence 44, Appl
39	865	81.5	195	4	US-09-224-681-44	Sequence 44, Appl
40	862.5	81.3	274	4	US-08-482-918-51	Sequence 51, Appl
41	862.5	81.3	274	4	US-09-224-681-51	Sequence 51, Appl
42	862.5	81.3	274	4	US-08-336-728A-51	Sequence 51, Appl
43	861	81.1	273	4	US-08-482-918-42	Sequence 42, Appl
44	861	81.1	273	4	US-09-224-681-42	Sequence 42, Appl
45	861	81.1	273	4	US-08-336-728A-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-836-252A-6
Sequence 6, Application US/08836252A
Patent No. 6177556

GENERAL INFORMATION:

APPLICANT: Sharkey, Andrew M.

APPLICANT: Smith, Stephen K.

APPLICANT: Dellow, Kimberley A.

TITLE OF INVENTION: HUMAN SCF, A SPLICED VARIANT THEREOF, ITS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESSES:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836, 252A

FILING DATE: 31-JULY-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO PCT/GB95/02547

FILING DATE: 31-OCT-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9422293.2

FILING DATE: 04-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9508618.7

FILING DATE: 28-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: ROBERT W. ESMOND

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0623.0550000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 208 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-836-252a-6

Query Match 100.0%; Score 1061; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.3e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
QY 121 KDLKSKSPERPLFTPEEFRIENRSIDAFKDFVAVASETSDCVVSSSTLSPKDSRVSVT 180
DB 121 KDLKSKSPERPLFTPEEFRIENRSIDAFKDFVAVASETSDCVVSSSTLSPKDSRVSVT 180
QY 181 KPFLPVAASLRNDSSSNKXYILI 208
DB 181 KPFLPVAASLRNDSSSNKXYILI 208

RESULT 2

US-08-482-918-46
; Sequence 46, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-46

Query Match 100.0%; Score 1061; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.3e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60

DB 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60

QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVNIYDDLVECKENSS 120

QY 121 KDLKSKSPERPLFTPEEFRIENRSIDAFKDFVAVASETSDCVVSSSTLSPKDSRVSVT 180
DB 121 KDLKSKSPERPLFTPEEFRIENRSIDAFKDFVAVASETSDCVVSSSTLSPKDSRVSVT 180

QY 181 KPFLPVAASLRNDSSSNKXYILI 208
DB 181 KPFLPVAASLRNDSSSNKXYILI 208

RESULT 3

US-09-224-681-46
; Sequence 46, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300

APPLICATION NUMBER: 07/422,383

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: cleavage site
LOCATION: 164...165
US-08-220-379B-2

Query Match 97.1% Score 1030; DB 1; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISEMVOVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVCEVKENS 120
DB 61 MDVLPSCWISEMVOVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVCEVKENS 120
QY 121 KDLKSKFSPEPRLPTEPEFRIFNRSIDAFKDVVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSPEPRLPTEPEFRIFNRSIDAFKDVVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSNRK 203
DB 181 KPFMLPPVAASSLRNDSSSNRK 203

RESULT 6
US-08-628-428-9
Sequence 9, Application US/08628428
Patent No. 5885962

GENERAL INFORMATION:

APPLICANT: Lu, Hsieng
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..273
OTHER INFORMATION: /note="NOTE: Mature full length
OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
OTHER INFORMATION: recombinant SCF."

US-08-628-428-9

Query Match 97.1% Score 1030; DB 2; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISEMVOVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVCEVKENS 120
DB 61 MDVLPSCWISEMVOVQSDSLTDLDFKSNISEGLSNYSIIDKLVINIVDDLVCEVKENS 120
QY 121 KDLKSKFSPEPRLPTEPEFRIFNRSIDAFKDVVASSETSDCVSSTLSPKDSRVSVT 180
DB 121 KDLKSKFSPEPRLPTEPEFRIFNRSIDAFKDVVASSETSDCVSSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSNRK 203
DB 181 KPFMLPPVAASSLRNDSSSNRK 203

RESULT 7
US-08-482-918-48
Sequence 48, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:

APPLICANT: Zsedo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-48

Query Match 97.1% Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60

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Db 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNRVTNNVKVTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISEMNVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVECKENSS 120
Db 61 MDVLPSCWISEMNVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVECKENSS 120
QY 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
Db 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPMLPPVAASSLRNDSSSSNRK 203
Db 181 KPMLPPVAASSLRNDSSSSNRK 203

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RESULT 8
US-08-482-918-49
; Sequence 49, Application US/08482918
; Patent No. 6207417

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; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

```

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; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-482-918-49

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```

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNRVTNNVKVTKLVANLPKDYMITLKYVG 60
Db 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNRVTNNVKVTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISEMNVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVECKENSS 120
Db 61 MDVLPSCWISEMNVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVECKENSS 120

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QY 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
Db 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPMLPPVAASSLRNDSSSSNRK 203
Db 181 KPMLPPVAASSLRNDSSSSNRK 203

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RESULT 9
US-08-482-918-61
; Sequence 61, Application US/08482918
; Patent No. 6207417

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; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-482-918-61

```

```

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNRVTNNVKVTKLVANLPKDYMITLKYVG 60
Db 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNRVTNNVKVTKLVANLPKDYMITLKYVG 60

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QY 61 MDVLPSCWISEMNVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVECKENSS 120
Db 61 MDVLPSCWISEMNVVOLSLSLTDLDKFSNISSEGLSNYSIIDKLVINVDLVECKENSS 120
QY 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
Db 121 KDLKSFSPERPLFTPEEFRIFRNSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPMLPPVAASSLRNDSSSSNRK 203
Db 181 KPMLPPVAASSLRNDSSSSNRK 203

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RESULT 10
US-09-224-681-48
Sequence 48, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48
Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98; 1; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLPNDLVKTEGICRRNRYNNKDYTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLLPNDLVKTEGICRRNRYNNKDYTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISEMNVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
DB 61 MDVLPSCWISEMNVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY 121 KDLKRSKSPERPLFTEPEFRIRNRSIDAFKDFVVASFSDCVSSTLSPEKDSRYVT 180
DB 121 KDLKRSKSPERPLFTEPEFRIRNRSIDAFKDFVVASFSDCVSSTLSPEKDSRYVT 180
QY 181 KPFMLPVAASLNRNDSSSNSK 203
DB 181 KPFMLPVAASLNRNDSSSNSK 203
RESULT 11
US-09-224-681-49
Sequence 49, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYIQLLFPNPLVTEGICRNRVTNNKDYTKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWITLCIYIQLLFPNPLVTEGICRNRVTNNKDYTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYDDLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYDDLVECVKENS 120
QY 121 KDLKSEKSPPEPLFTPEEFRIINRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSEKSPPEPLFTPEEFRIINRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPPVAASSLRNDSSSSNSK 203

RESULT 12

US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454

GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/962,255
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-61

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYIQLLFPNPLVTEGICRNRVTNNKDYTKLVANLPKDYMITLKYVG 60
DB 1 MKKTQWITLCIYIQLLFPNPLVTEGICRNRVTNNKDYTKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISSEMYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYDDLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVNIYDDLVECVKENS 120
QY 121 KDLKSEKSPPEPLFTPEEFRIINRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
DB 121 KDLKSEKSPPEPLFTPEEFRIINRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSSNSK 203
DB 181 KPFMLPPVAASSLRNDSSSSNSK 203

RESULT 13

US-08-336-728A-48
Sequence 48, Application US/08336728A
Patent No. 6207802

GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/336,728A
;; FILING DATE: 09-NOV-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/982,255
;; FILING DATE: 25-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/589,701
;; FILING DATE: 01-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/573,616
;; FILING DATE: 24-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/537,198
;; FILING DATE: 11-JUN-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/422,383
;; FILING DATE: 16-OCT-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clough, David W.
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 01017/32956
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELETYPE: 25-3856
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 273 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-336-728A-48

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKQTQWILTCIYQILLFNPVLTGEGICRRNRYNNVKDVKLVANLPKQYMITLKYVG 60
Db 1 MKQTQWILTCIYQILLFNPVLTGEGICRRNRYNNVKDVKLVANLPKQYMITLKYVG 60

QY 61 MDVLPSCWISEMNVQSLDLDLDFKSNISGLSNYSIIDKLVNIYVDLVKCVKENS 120
Db 61 MDVLPSCWISEMNVQSLDLDLDFKSNISGLSNYSIIDKLVNIYVDLVKCVKENS 120

QY 121 KDILKSKSPERPLFTPEEFRIENRSIDAFKDPVVAASETSDCVSSTLSPEKDSRVSVT 180
Db 121 KDILKSKSPERPLFTPEEFRIENRSIDAFKDPVVAASETSDCVSSTLSPEKDSRVSVT 180

QY 181 KPFMLPVAASSLRNDSSSSNRK 203
Db 181 KPFMLPVAASSLRNDSSSSNRK 203

RESULT 14
US-08-336-728A-49
; Sequence 49, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

;;
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/336,728A
;; FILING DATE: 09-NOV-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/982,255
;; FILING DATE: 25-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/589,701
;; FILING DATE: 01-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/573,616
;; FILING DATE: 24-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/537,198
;; FILING DATE: 11-JUN-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/422,383
;; FILING DATE: 16-OCT-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clough, David W.
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 01017/32956
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELETYPE: 25-3856
;; INFORMATION FOR SEQ ID NO: 49:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 273 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-336-728A-49

Query Match 97.1%; Score 1030; DB 4; Length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKQTQWILTCIYQILLFNPVLTGEGICRRNRYNNVKDVKLVANLPKQYMITLKYVG 60
Db 1 MKQTQWILTCIYQILLFNPVLTGEGICRRNRYNNVKDVKLVANLPKQYMITLKYVG 60

QY 61 MDVLPSCWISEMNVQSLDLDLDFKSNISGLSNYSIIDKLVNIYVDLVKCVKENS 120
Db 61 MDVLPSCWISEMNVQSLDLDLDFKSNISGLSNYSIIDKLVNIYVDLVKCVKENS 120

QY 121 KDILKSKSPERPLFTPEEFRIENRSIDAFKDPVVAASETSDCVSSTLSPEKDSRVSVT 180
Db 121 KDILKSKSPERPLFTPEEFRIENRSIDAFKDPVVAASETSDCVSSTLSPEKDSRVSVT 180

QY 181 KPFMLPVAASSLRNDSSSSNRK 203
Db 181 KPFMLPVAASSLRNDSSSSNRK 203

RESULT 15
US-08-336-728A-61
; Sequence 61, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.

Search completed: August 18, 2002, 13:04:01
Job time: 166 sec

APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-61

Query Match 97.1%; Score 1030; DB 4; length 273;
Best Local Similarity 99.5%; Pred. No. 3e-98;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKKTQWILTCIYIOLLFNPVKTGICRNVTNNVKVANKVANKVMTLTKYVG 60
DB 1 MKKTQWILTCIYIOLLFNPVKTGICRNVTNNVKVANKVANKVMTLTKYVG 60
QY 61 MDVLPSCWISSEMYVQLSDSLDLDFKFSNISSEGISNYSIIDKLVINIYDDIVECYKENSS 120
DB 61 MDVLPSCWISSEMYVQLSDSLDLDFKFSNISSEGISNYSIIDKLVINIYDDIVECYKENSS 120
QY 121 KDLKSKFSPEPRLFTPEEFRIFRNSIDAFKDFYVASSETSDCVVSTLSPEKDSRVSVT 180
DB 121 KDLKSKFSPEPRLFTPEEFRIFRNSIDAFKDFYVASSETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPEMLPVVAASLRNDSSSSNSK 203
DB 181 KPEMLPVVAASLRNDSSSSNSK 203

Sun Aug 18 14:09:01 2002

us-09-604-325a-46.rai

Page 10

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 62.73 Seconds

(Without alignments)
318.613 Million cell updates/sec

Title: US-09-604-325a-46

Sequence: 1 MKKTQWILTCIYLQLLEFN.....AASLRNDSSNSKYLIL 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1030	97.1	273	A35974	mast cell growth f
2	899.5	84.8	274	I46575	c-kit ligand - pig
3	890	83.9	245	B61190	mast cell growth f
4	886.5	83.6	274	S47571	stem cell factor
5	885.5	83.5	202	S58313	stem cell factor
6	862.5	81.3	274	I46929	stem cell factor
7	857	80.8	201	B35974	stem cell factor
8	855	80.6	273	S65801	stem cell factor
9	715	67.4	245	A37934	mast cell growth f
10	576.5	54.3	124	S29052	mast cell growth f
11	570.5	53.8	287	S70366	stem cell factor
12	562.5	53.0	287	JN0637	stem cell factor
13	479.5	45.2	253	S70367	stem cell factor
14	175.5	16.5	51	B35971	stem cell factor
15	172.5	16.3	49	A35971	stem cell growth f
16	97.5	9.2	1490	I46086	hypothetical prote
17	97	9.1	1447	T16086	hypothetical prote
18	94	8.9	1293	T27886	hypothetical prote
19	94	8.9	1813	T19295	hypothetical prote
20	92.5	8.7	164	B69616	cell-division init
21	92.5	8.7	512	C66773	clatrate (pro-35)-1
22	92	8.7	935	S63261	SEC21 protein - ye
23	91	8.6	1107	S61667	probable membrane
24	90.5	8.5	616	A69136	ATP-dependent GTP
25	89	8.4	1734	A41101	phorbol ester-bind
26	88.5	8.3	545	B44054	orf2 protein - Jun
27	88.5	8.3	941	B44855	phosphoenolpyruvat
28	88	8.3	335	S44922	K18 antigen - Enta
29	88	8.3	465	H97165	flagellar hook-len

30	88	8.3	702	F97352	membrane-associate
31	88	8.3	1690	T31670	DNA-directed RNA p
32	87.5	8.2	649	T04005	probable protein k
33	87.5	8.2	966	S26235	phosphoenolpyruvat
34	87	8.2	664	T16411	hypothetical prote
35	86.5	8.2	246	T19850	hypothetical prote
36	86.5	8.2	436	F86486	hypothetical prote
37	86.5	8.2	844	S61104	protein F28J9.3 (1
38	86.5	8.2	1271	T08607	BRO1 protein - yea
39	86	8.1	246	A64579	hypothetical prote
40	86	8.1	496	T23794	molybdenum ABC tra
41	86	8.1	660	T23794	theonine synthase
42	86	8.1	1334	T18493	hypothetical prote
43	85.5	8.1	222	T23762	hypothetical prote
44	85.5	8.1	614	B86461	probable protein k
45	85.5	8.1	636	A45949	merozoite surface

ALIGNMENTS

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mast cell growth factor precursor - human
N:Alternate names: Kit ligand, stem cell factor
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: A35974; A61190
S:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris,
S, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev
Cell 63, 203-211, 1990
A>Title: Primary structure and functional expression of rat and human stem cell facto
A:Reference number: A35974; MUID:91004219
A:Accession: A35974
A:Molecule type: mRNA
A:Residues: 1-273 <MAR>
A:Cross-references: GB:M5964; NID:q337933; PIDN:AAA8450.1; PID:q337934
R:Anderson, D.M.; Williams, D.E.; Tushnetski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro
Cell Growth Differ. 2: 373-378, 1991
A>Title: Alternate splicing of mRNAs encoding human mast cell growth factor and local
A:Reference number: A61190; MUID:92177791
A:Accession: A61190
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
A:Gene: GDB:MCF
A:Cross-references: GDB:128026; OMIM:184745
A:Map position: 12q22-12q22
C:Superfamily: mouse mast cell growth factor
C:Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-273/Product: mast cell growth factor #status predicted <MCS>
F:26-188/Product: (or 26-190) mast cell growth factor, soluble form #status predicted
F:215-237/Domain: transmembrane #status predicted <TM>
F:90,97,118,145,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          97.1%  Score 1030; DB 2; Length 273;
Best Local Similarity 99.5%  Pred. No. 3.7e-75;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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1 MKKTQWILTCIYLQLLEFNPLVTEGICRNRYNNKVDYTKLVANPKDYMITLKVP 60
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MDVPSHCWISSEMYVSDSITDLDFKFSNISSEGLSNYSIIDKLVINIVDDLVCEVKNSS 120
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KDLKSKSPSPRLFTPEEFRIFFNRSIDAFKDFVAVASESDCVSSTLSPKDSVSV 180
KDLKSKSPSPRLFTPEEFRIFFNRSIDAFKDFVAVASESDCVSSTLSPKDSVSV 180
KDLKSKSPSPRLFTPEEFRIFFNRSIDAFKDFVAVASESDCVSSTLSPKDSVSV 180

Qy 181 KPFLPVAASSLRNDSSSSNRK 203
 Db 181 KPFLPVAASSLRNDSSSSNRK 203

RESULT 2
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 c-kit ligand - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: 146575
 R:Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
 A:Reference number: 146575; MUID:94146218
 A:Accession: 146575
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-274 <2HA>
 A:Cross-references: GB:L07786; NID:g164420; PIDN:AAA53670.1; PID:g164421
 C:Superfamily: mouse mast cell growth factor

Query Match 84.8%; Score 899.5; DB 2; Length 274;
 Best Local Similarity 86.3%; Pred. No. 1e-64;
 Matches 176; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MKKTQWITLCIYIQLLFNPLVKTGICRNRVNNVADTKLVANLPKDYMITLKYVG 60
 Db 1 MKKTQWITLCIYIQLLFNPLVKTGICRNRVNNVADTKLVANLPKDYMITLKYVG 60
 Qy 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Qy 121 KDLSKFSPEPRLEPTPEEFRIENRSIDAFKDF-VVASSETSDCVVSTLSPEKDSRVSV 179
 Db 121 ENVKSSKSPERLFTPEKFGIFNRSIDAFKDLVMAKSECVISSTLPEKDSRVSV 180
 Qy 180 TKPFMLPVAASSLRNDSSSSNRK 203
 Db 181 TKPFMLPVAASSLRNDSSSSNRK 204

RESULT 3
 B61190
 mast cell growth factor, short form precursor - human
 N:Alternate names: kit ligand, short form; stem cell factor, short form
 C:Species: Homo sapiens (man)
 C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
 C:Accession: B61190
 R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, L.
 Cell Growth Differ. 2, 373-378, 1991
 A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localized
 A:Reference number: B61190; MUID:92172791
 A:Accession: B61190
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-245 <AND>
 A:Comment: Alternative splicing produces this short form in which a predicted cleavage
 C:Genetics:
 A:Gene: GDB:MGF
 A:Cross-references: GDB:128026; OMIM:184745
 A:Map position: 12q22-12q22
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:187-209/Domain: transmembrane #status predicted <TMN>
 F:90,97,118,145/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 83.9%; Score 890; DB 2; Length 245;

Best Local Similarity 100.0%; Pred. No. 5.1e-64;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKTQWITLCIYIQLLFNPLVKTGICRNRVNNVADTKLVANLPKDYMITLKYVG 60
 Db 1 MKKTQWITLCIYIQLLFNPLVKTGICRNRVNNVADTKLVANLPKDYMITLKYVG 60
 Qy 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Qy 121 KDLSKFSPEPRLEPTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPEK 173
 Db 121 KDLSKFSPEPRLEPTPEEFRIENRSIDAFKDFVVASSETSDCVVSTLSPEK 173

RESULT 4
 S47571
 stem cell factor, longer isoform - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S47571
 R:Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
 Biochim. Biophys. Acta 1223, 148-150, 1994
 A:Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine
 A:Reference number: S47571; MUID:94339176
 A:Accession: S47571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-274 <2HO>
 A:Cross-references: EMBL:D28934; NID:g538520; PIDN:BA006061.1; PID:g538521
 C:Superfamily: mouse mast cell growth factor

Query Match 83.6%; Score 886.5; DB 2; Length 274;
 Best Local Similarity 85.3%; Pred. No. 1.1e-63;
 Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

Qy 1 MKKTQWITLCIYIQLLFNPLVKTGICRNRVNNVADTKLVANLPKDYMITLKYVG 60
 Db 1 MKKTQWITLCIYIQLLFNPLVKTGICRNRVNNVADTKLVANLPKDYMITLKYVG 60
 Qy 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQSDSLDLDKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Qy 121 KDLSKFSPEPRLEPTPEEFRIENRSIDAFKDF-VVASSETSDCVVSTLSPEKDSRVSV 179
 Db 121 ENVKSSKSPERLFTPEKFGIFNRSIDAFKDLVMAKSECVISSTLPEKDSRVSV 180
 Qy 180 TKPFMLPVAASSLRNDSSSSNRK 203
 Db 181 TKPFMLPVAASSLRNDSSSSNRK 204

RESULT 5
 S58313
 stem cell factor precursor - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
 C:Accession: S58313
 R:McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
 Submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and biological activity of ovine stem cell factor.
 A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MC1>
 A:Cross-references: EMBL:Z50743; NID:g940807; PIDN:CAA90620.1; PID:g940808
 C:Superfamily: mouse mast cell growth factor


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A:Accession: A35977; MUID:91004223
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-273 <AND>
A:Cross-references: GB:M57647; GB:M38436; NID:g199151; PIDN:AAA9358.1; PID:g199152
R:Coppeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.; An
Cell 63, 175-183, 1990
A:Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and is
A:Reference number: A35972; MUID:91004216
A:Accession: A35972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 26-53 <COP>
A:Cross-references: GB:M59912
R:Zebo, K.M.; Williams, D.A.; Geisler, E.N.; Broudy, V.C.; Martin, F.H.; Atkins, H.L.;
Cattanch, B.M.; Gall, S.J.; Suggs, S.V.
Cell 63, 213-224, 1990
A:Title: Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for
A:Reference number: A35975; MUID:91004220
A:Accession: A35975
A:Molecule type: mRNA
A:Residues: 1-201 <RES>
A:Cross-references: GB:M59915; NID:g200935; PIDN:AAA0095.1; PID:g554271
R:Zebo, K.M.; Wpych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
A:Langley, R.E.
Cell 63, 195-201, 1990
A:Title: Identification, purification, and biological characterization of hematopoietic
A:Reference number: A35973; MUID:91004218
A:Accession: A35973
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-29, 'R', 31-39 <ES2>
R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.;
Genes Dev. 6, 1832-1842, 1992
A:Title: Developmental abnormalities in Steel17h mice result from a splicing defect in t
A:Reference number: A44071; MUID:93012940
A:Accession: 148768
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206, 'S', 208-273 <RES>
A:Cross-references: EMBL:X68989; NID:g395283; PIDN:CAA48778.1; PID:g395284
C:Genetics:
A:Gene: Slf
A:Map position: 10
C:Superfamily: mouse mast cell growth factor
C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query Match      80.6%; Score 855; DB 2; Length 273;
Best Local Similarity 82.3%; Pred. No.3.7e-61;
Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

OY 1 MKRTQWILTCIYDQLLEFNPLVKTGEGICRNFVNNKVDYTKLVANLPKDYITLTKYPG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MKRTQWITTCIYDQLLEFNPLVKTGEGICRNFVNNKVDYTKLVANLPNDYMITLTINYAG 60
OY 61 MVLVSHOCISMVWVQSLFDLIDKFSNISSEGLSNYSIIDKLVINVDLVECYKENS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 MVLVSHOCILRMVQIQLSLITLIDKFSNISSEGLSNYSIIDKLVINVDLVECHENAP 120
OY 121 KDLKSFSPPERLTPEEFRIFNKSIDAFKDFVAVASETSCVYSSSTLSPKDSRVSVT 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 KNIKSPKPEPRTSPTEPEEFISFNKSIDAFKDFVAVASPTSDCVLSTLGPKDSRVSVT 180
OY 181 KPFMLPPVAASSLRNDSSSNK 203
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 KPFMLPPVAASSLRNDSSSNRK 203

RESULT      9
A37934
mast cell growth factor precursor (version 2) - mouse

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N:Alternate names: KL-2 protein
C:Species: *Mus musculus* (house mouse)
C:Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
C:Accession: A37934; B43751
R:Flanagan, J.G.; Chan, D.C.; Leder, P.
Cell 64, 1025-1035, 1991
A:Title: Transmembrane form of the kit ligand growth factor is determined by alternat
A:Reference number: A37934; MUID:91160046
A:Accession: A37934
A:Molecule type: mRNA
A:Residues: 1-245 <FLA>
A:Cross-references: GB:M64262
R: Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A:Title: Differential expression and processing of two cell associated forms of the k
A:Reference number: A43751; MUID:92330001
A:Accession: B43751
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-173, 'R', '175-186', 'L', '188-245 <HUA>
A:Cross-references: GB:S04534
A:Note: the authors translated the codon TTG for residue 187 as Trp
C:Superfamily: mouse mast cell growth factor

Query Match	67.4%	Score 715	DB 2	Length 245	
Best Local Similarity	79.8%	Pred. No. 5.2e-50			
Matches 138	Conservative 16	Mismatches 19	Indels 0	Gaps 0	
QY	1	MKKTQWTILTCIYIQLLEFNPLVKTGICRNRVYTNVKNVDTKLVANLPKDYMITLKYPG	60		
DB	1	MKKQTWITITCIYQLLEFNPLVKTGICGNPVTDNVKNIDTKLVANLPNDYMITLNVAG	60		
QY	61	MDVPSHCHISMVAVQSLDSTLTDLDKFSNISEGINSIIDKLVIYDDIVECKENSS	120		
DB	61	MDVPSHCHLRMVAVQLSLSTLTLDKFSNISEGINSIIDKLKTYDDLVLCHEENAP	120		
QY	121	KDLKSEFKSPPEPRLTPEEFERIFNRSIDAFKDFVASETSQVVSSTLSPEK	173		
DB	121	KNKESPKRPFERSTPEEFESIFNRSIDAFKDFVAVASDTSCVLSSTLGEK	173		
RESULT	10				
S29052		stem cell factor - human (fragments)			
C.Species:		Homo sapiens (man)			
C.Date:		22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000			
C.Accession:		S29052			
R.Liv, H.S.;		Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderak, K.; Balte			
Arch. Biochem. Biophys.		298, 150-158, 1992			
A.Title:		Post-translational processing of membrane-associated recombinant human stem			
A.Reference number:		S29052; MUID:92398336			
A.Accession:		S29052			
A.Status:		preliminary			
A.Molecule type:		protein			
A.Residues:		1-131;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUD>			
C:Superfamily:		mouse mast cell growth factor			
Query Match	54.3%	Score 576.5	DB 2	Length 124	
Best Local Similarity	75.2%	Pred. No. 2.7e-39			
Matches 124	Conservative 0	Mismatches 0	Indels 41	Gaps 4	
QY	26	EGICRRRVNNVKNQDYKTLVANLPKDYMITLKYPGMDVLPSSHCHWISENVVQLSDSLTDL	85		
DB	1	EGICRRRVNNVK-----DVLPSSHCHWISENVVQLS-----	30		
QY	86	DKFSNISEGINSIIDKLVIYDDIVECKENSSKDLKSKSPPEPRLTPEEFERIFN	145		
DB	31	DKFSNISEGINSYII-----DDLVECKENSSKDLKSKSPPEPRLTPEEFERIFN	83		
QY	146	RSTDAKDFDVAVASETSQVVSSTLSPEKDSRVSVTKPFLMPVAA	190		

Db 84 RSI-----DFVASETSDCVVSTLSPKDSRVSTKPFMLPPVAA 124

RESULT 11

S70367
stem cell factor long form precursor - qual1
C:Species: Coturnix coturnix (quail)
C>Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Accession: S70366
R:Petite, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fac
A:Reference number: S70366; MUID:96283808
A:Accession: S70366
A:Molecule type: mRNA
A:Residues: 1-287 <P>
A:Cross-references: EMBL:U43078; NID:g1150875; PIDN:AAC59933.1; PID:g1150876
C:Superfamily: mouse mast cell growth factor
C:Keywords: growth factor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-287/Product: stem cell factor long form #status predicted <MAT>
F:226-250/Domain: transmembrane #status predicted <TM>

Query Match 53.8%; Score 570.5; DB 2; Length 287;
Best Local Similarity 55.1%; Pred. No. 2.4e-38;
Matches 114; Conservative 37; Mismatches 51; Indels 5; Gaps 3;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRVNNVADVRLVANKPKDYMILTKYVP 60
1 MKKAQTWITTCFCLQLLLNPLVKTGSSCGNPVTDVNDIAKLVGNLPNDYLITLKYVP 60
Db 1 MDLSPHNCWHLMAVPEFSRLHNLQKFDVSDMSVLSNYSIINNLTITINDMACLAF 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKF---SNISEGLSNYSITDKLVNIIVDLVCEYK 117
1 MDLSPHNCWHLMAVPEFSRLHNLQKFDVSDMSVLSNYSIINNLTITINDMACLAF 120
Db 61 MDLSPHNCWHLMAVPEFSRLHNLQKFDVSDMSVLSNYSIINNLTITINDMACLAF 120
QY 118 NSSKD-LKSKFSPEPRLTPEEFRIIFNRSIDAFKDFVAVSETSDCVVSTL-SPKDS 175
121 DKKNDFIKENGHLVEDRFIDENFRLFNRTIEVYKEFADSLDKNDICIMPSTVETPEN 180
Db 121 DKKNDFIKENGHLVEDRFIDENFRLFNRTIEVYKEFADSLDKNDICIMPSTVETPEN 180
QY 176 RVSVTKPFMLPPVAAASLRNDSSNS 202
181 RAVATKTIISFPVAAASLRNDSSNS 207
Db 181 RAVATKTIISFPVAAASLRNDSSNS 207

RESULT 12

JN0637
stem cell factor precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0637
R:Zhou, J.H.; Ohtaki, M.; Sakurai, M.
Gene 127, 269-270, 1993
A:Title: Sequence of a cDNA encoding chicken stem cell factor.
A:Reference number: JN0637; MUID:93273244
A:Accession: JN0637
A:Molecule type: mRNA
A:Residues: 1-287 <ZHO>
A:Cross-references: GB:DJ3516; NID:g391648; PIDN:BA002733.1; PID:g391649
A:Experimental source: brain
C:Superfamily: mouse mast cell growth factor
C:Keywords: growth factor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-287/Product: stem cell factor #status predicted <MAT>
F:226-248/Domain: transmembrane #status predicted <TM>

Query Match 53.0%; Score 562.5; DB 2; Length 287;
Best Local Similarity 54.6%; Pred. No. 1e-37;
Matches 113; Conservative 36; Mismatches 53; Indels 5; Gaps 3;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRVNNVADVRLVANKPKDYMILTKYVP 60

Db 1 MKKAQTWITTCFCLQLLLNPLVKAQSSCGNPVTDVNDIAKLVGNLPNDYLITLKYVP 60

QY 61 MDVLPSCWISSEWVQSDSLTDLDKFSNI---SEGLSNYSITDKLVNIIVDLVCEYK 117
1 MDLSPHNCWHLMAVPEFSRLHNLQKFDVSDMSVLSNYSIINNLTITINDMACLAF 120
Db 61 MDLSPHNCWHLMAVPEFSRLHNLQKFDVSDMSVLSNYSIINNLTITINDMACLAF 120

QY 118 NSSKD-LKSKFSPEPRLTPEEFRIIFNRSIDAFKDFVAVSETSDCVVSTL-SPKDS 175
121 DKKNDFIKENGHLVEDRFIDENFRLFNRTIEVYKEFADSLDKNDICIMPSTVETPEN 180
Db 121 DKKNDFIKENGHLVEDRFIDENFRLFNRTIEVYKEFADSLDKNDICIMPSTVETPEN 180

QY 176 RVSVTKPFMLPPVAAASLRNDSSNS 202
181 RAVATKTIISFPVAAASLRNDSSNS 207
Db 181 RAVATKTIISFPVAAASLRNDSSNS 207

RESULT 13

S70367
stem cell factor short form precursor - qual1
C:Species: Coturnix coturnix (quail)
C>Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Accession: S70367
R:Petite, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell
A:Reference number: S70366; MUID:96283808
A:Accession: S70367
A:Molecule type: mRNA
A:Residues: 1-253 <P>
A:Cross-references: EMBL:U43079; NID:g1150877; PIDN:AAC59934.1; PID:g1150878
C:Superfamily: mouse mast cell growth factor
C:Keywords: growth factor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-253/Product: stem cell factor short form #status predicted <MAT>
F:192-216/Domain: transmembrane #status predicted <TM>

Query Match 45.2%; Score 479.5; DB 2; Length 253;
Best Local Similarity 46.9%; Pred. No. 3.9e-31;
Matches 100; Conservative 42; Mismatches 58; Indels 13; Gaps 4;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRVNNVADVRLVANKPKDYMILTKYVP 60
1 MKKAQTWITTCFCLQLLLNPLVKTGSSCGNPVTDVNDIAKLVGNLPNDYLITLKYVP 60
Db 1 MDLSPHNCWHLMAVPEFSRLHNLQKFDVSDMSVLSNYSIINNLTITINDMACLAF 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDKF---SNISEGLSNYSITDKLVNIIVDLVCEYK 117
1 MDLSPHNCWHLMAVPEFSRLHNLQKFDVSDMSVLSNYSIINNLTITINDMACLAF 120
Db 61 MDLSPHNCWHLMAVPEFSRLHNLQKFDVSDMSVLSNYSIINNLTITINDMACLAF 120
QY 118 NSSKD-LKSKFSPEPRLTPEEFRIIFNRSIDAFKDFVAVSETSDCVVSTL-SPKDS 175
121 DKKNDFIKENGHLVEDRFIDENFRLFNRTIEVYKEFADSLDKNDICIMPSTVETPEN 180
Db 121 DKKNDFIKENGHLVEDRFIDENFRLFNRTIEVYKEFADSLDKNDICIMPSTVETPEN 180
QY 176 RVSVTKPFMLPPVAAASLRNDSSNS 208
181 ALGF-----ISSSLQGISIALTSLISLI 205
Db 181 ALGF-----ISSSLQGISIALTSLISLI 205

RESULT 14

B35971
mast cell growth factor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:Accession: B35971
R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park
Cell 63, 167-174, 1990
A:Title: Identification of a ligand for the c-kit proto-oncogene.
A:Reference number: A35971; MUID:91004215
A:Accession: B35971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-51 <WIL>
C:Superfamily: mouse mast cell growth factor

Query Match 45.2%; Score 479.5; DB 2; Length 253;
Best Local Similarity 46.9%; Pred. No. 3.9e-31;
Matches 100; Conservative 42; Mismatches 58; Indels 13; Gaps 4;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRVNNVADVRLVANKPKDYMILTKYVP 60

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 35.93 Seconds
(Without alignments) 224.149 Million cell updates/sec

Title: US-09-604-325a-46
Perfect score: 1061
Sequence: 1 MKKTQWILTCIYLQLLFN.....AASLRNDSNSSKTYILI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1030	97.1	273	1	SCF_HUMAN
2	899.5	84.8	274	1	SCF_PIG
3	862.5	81.3	274	1	SCF_CANFA
4	857	80.8	201	1	SCF_RAT
5	855	80.6	273	1	SCF_MOUSE
6	562.5	53.0	287	1	SCF_CHICK
7	102	9.6	981	1	SCA4_RICFA
8	92	8.7	935	1	COG_YEAST
9	90.5	8.5	1742	1	MYSC_HUMAN
10	89	8.4	989	1	PRP3_DICDI
11	89	8.4	1815	1	UN13_CAEEL
12	88.5	8.3	545	1	VNCS_JCDNY
13	87.5	8.2	966	1	CAPP_MEDSA
14	87	8.2	664	1	2AAA_CAEEL
15	86.5	8.2	844	1	BRO1_YEAST
16	84.5	8.0	466	1	DNAA_PROMT
17	84.5	8.0	964	1	CAPP_TOBAC
18	84.5	8.0	998	1	SCA4_RICAK
19	82.5	7.8	451	1	DNAA_PASMO
20	82.5	7.8	991	1	SCA4_RICAU
21	82	7.7	1140	1	YMG6_YEAST
22	82	7.7	1188	1	PSA_METUA
23	82	7.7	1224	1	MSN5_YEAST
24	81	7.6	196	1	KITH_YEAST
25	81	7.6	388	1	YAS5_METUA
26	81	7.6	490	1	CPOK_MACFA
27	80.5	7.6	373	1	BIOF_HELPJ
28	80.5	7.6	442	1	YUBI_ECOLI
29	80.5	7.6	755	1	P100_HSVJ7
30	80.5	7.6	2238	1	RRLI_BUNYW
31	80.5	7.6	4563	1	APB_HUMAN
32	80	7.5	480	1	YB9Q_YEAST
33	80	7.5	490	1	CPC8_HUMAN

34	79.5	7.5	447	1	DNAA_SYNY3	P49995 synecocyst
35	79.5	7.5	455	1	DNAA_LACIA	O9C1J2 lactococcus
36	79.5	7.5	540	1	AXR1_ARATH	P42744 arabidopsis
37	79.5	7.5	640	1	UL06_HSVJ7	P52455 human herpes
38	79.5	7.5	729	1	CUR6_CAEEL	O21346 caenorhabdi
39	79.5	7.5	737	1	SUV3_YEAST	P32580 saccharomyc
40	79.5	7.5	966	1	CAP1_MESCR	P10490 mesembryant
41	79.5	7.5	1294	1	YASB_SCHPO	O09716 schizosacch
42	79	7.4	420	1	YMS7_YEAST	O03694 saccharomyc
43	79	7.4	2492	1	TALA_DICDI	P54633 dictyosteli
44	78.5	7.4	166	1	INC_MARMO	O35735 marmota mon
45	78.5	7.4	229	1	YSV4_CAEEL	Q10010 caenorhabdi

ALIGNMENTS

RESULT	1	STANDARD	PRT	273 AA
ID	SCF_HUMAN			
AC	P21583			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
GN	KITLG OR MGF OR SCF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=91004219; Pubmed=2208279;			
RA	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,			
RA	Morris C.F., McNeice I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,			
RA	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,			
RA	Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sacdev R.K.,			
RA	Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;			
RT	"Primary structure and functional expression of rat and human stem cell factor DNAs."			
RL	Cell 63:203-211(1990).			
CC	-!- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH WEIROID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES. PROBABLY INTERLEUKINS.			
CC	-!- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).			
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.			
CC	-!- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.			
CC	-!- SIMILARITY: BELONGS TO THE SCF FAMILY.			
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CC	EMBL: M59964; AAA85450.1; -.			
DR	PIR: A35974; A35974.			
DR	MIM: 184745; -.			
DR	InterPro: IPR003452; SCF.			
DR	Pfam: PF02404; SCF. 1.			
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.			
FT	SIGNAL	1	25	
FT	CHAIN	26	273	
FT	DOMAIN	26	214	
FT	TRANSSEM	215	237	
FT	DOMAIN	238	273	
FT	DISULFID	29	114	
FT	KIT LIGAND. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). BY SIMILARITY.			

FT DISULFID 68 163 BY SIMILARITY
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 273 AA; 30898 MW; 19FD362CB596607 CRC64;

Query Match Best Local Similarity 97.1%; Score 1030; DB 1; Length 273;
 Pred. No. 1.4e-73;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKTOTWILTCIYQLLLFNPVLTGEGICRNRYNNVNDVKLVANLPKDYMITLKYPG 60
 DB 1 MKKTOTWILTCIYQLLLFNPVLTGEGICRNRYNNVNDVKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEWVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVIYDDLYECVKNSS 120
 DB 61 MDVLPSCWISSEWVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVIYDDLYECVKNSS 120
 QY 121 KDLKSKFSPEPRLTPEEFERFNRSIDAEKDFVAVASSETDCVVSSTLSEPKDSRVSVT 180
 DB 121 KDLKSKFSPEPRLTPEEFERFNRSIDAEKDFVAVASSETDCVVSSTLSEPKDSRVSVT 180
 QY 181 KPFMLPPVAASSLRNDSSSSNRK 203
 DB 181 KPFMLPPVAASSLRNDSSSSNRK 203

RESULT 2

SCF_PIG STANDARD; PRT; 274 AA.

AC 029030;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR MGF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=uterus;
 RX MEDLINE=94146218; PubMed=7508758;
 RA Zhang Z., Anthony R.V.;
 RT "Porcine stem cell factor/c-kit ligand: its molecular cloning and localization within the uterus.";
 RL Biol. Reprod. 50:95-102(1994).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
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 CC EMBL; L07786; AAA53670.1; -
 CC InterPro; IPR003452; SCF.
 CC Pfam; PF02404; SCF; 1.

KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.

FT SIGNAL 1 25 BY SIMILARITY.
 FT CHAIN 26 274 KIT LIGAND.
 FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 216 238 POTENTIAL.
 FT DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 29 114 BY SIMILARITY.
 FT DISULFID 68 164 BY SIMILARITY.
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 274 AA; 31118 MW; FFC387114D7BA6A6 CRC64;

Query Match Best Local Similarity 84.8%; Score 899.5; DB 1; Length 274;
 Pred. No. 2.1e-63;
 Matches 176; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

QY 1 MKKTOTWILTCIYQLLLFNPVLTGEGICRNRYNNVNDVKLVANLPKDYMITLKYPG 60
 DB 1 MKKTOTWILTCIYQLLLFNPVLTGEGICRNRYNNVNDVKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEWVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVIYDDLYECVKNSS 120
 DB 61 MDVLPSCWISSEWVQLSDSLTDLDFKFSNISSEGLSNYSIIDKLVIYDDLYECVKNSS 120
 QY 121 KDLKSKFSPEPRLTPEEFERFNRSIDAEKDFVAVASSETDCVVSSTLSEPKDSRVSVT 179
 DB 121 KDLKSKFSPEPRLTPEEFERFNRSIDAEKDFVAVASSETDCVVSSTLSEPKDSRVSVT 179
 QY 121 ENVAKSSKSPPEPRLTPEEFERFNRSIDAEKDFVAVASSETDCVVSSTLSEPKDSRVSVT 180
 DB 181 KPFMLPPVAASSLRNDSSSSNRK 204

RESULT 3

SCF_CANFA STANDARD; PRT; 274 AA.

AC 006220;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
 GN KITLG OR MGF.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=93106145; PubMed=1281786;
 RA Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W., Martin F.H.;
 RT "Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture.";
 RL Exp. Hematol. 20:1118-1124(1992).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
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CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).

DR EMBL: S53329; AAB24619.1; -
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF, 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 274
FT DOMAIN 26 274
FT TRANSMEM 216 215
FT DOMAIN 239 274
FT DISULFID 29 114
FT CARBOHYD 68 164
FT CARBOHYD 90 90
FT CARBOHYD 145 145
FT CARBOHYD 196 196
SQ SEQUENCE 274 AA; 30869 MW; 4182BE9AED00793B CRC64;
BY SIMILARITY.
KIT LIGAND.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 81.3%; Score 862.5; DB 1; Length 274;
Best Local Similarity 84.8%; Pred. No. 1.6e-60;
Matches 173; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

OY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNKDVTKLVANLPKDWITLKYVG 60
DB 1 MKKTQWITTCIYLQLLFNPLVKTGICRNVTNNKDVTKLVANLPKDWITLKYVG 60
OY 61 MDVLPSCHEWISVMVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
DB 61 MDVLPSCHEWISVMVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
OY 121 KDLKSKFSKSPERLFTPEEFRIENRSDAFKDF-VVASNSDCVVSSTLSPKDSRVSV 179
DB 121 EVVKAPKSPERLFTPEEFRIENRSDAFKDF-VVASNSDCVVSSTLSPKDSRVSV 180
OY 180 TKPFMLPVAASLRNDSSSSNSK 203
DB 181 TKPFMLPVAASLRNDSSSSNSK 204

RESULT 4
SCF_RAT STANDARD; PRT; 201 AA.
AC P21581;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF) (Fragment).
GN KITLG OR MGF.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]

RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=91004219; PubMed=2208279.
RA Martin F.H., Sugis S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
RA Morris C.F., McInce I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
RA Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
RA Fisher E.F., Eljavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
RT "Primary structure and functional expression of rat and human stem
RT cell factor DNAs."
RL Cell 63:203-211(1990).
[2]

RP SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RC STAIN-BUFFALO; TISSUE=Liver;
RX MEDLINE=91217037; PubMed=1708771;

RA Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
RA Mendiaz E.A., Zsebo K.M., Langley K.E.;
RT "Amino acid sequence and post-translational modification of stem cell
RT factor isolated from buffalo rat liver cell-conditioned medium."
RL J. Biol. Chem. 266:8102-8107(1991).
[3]

RP SEQUENCE OF 26-39.
RX MEDLINE=91004218; PubMed=2208278.
RA Zsebo K.M., Wypych J., McInce I.K., Lu H.S., Smith K.A.,
RA Karkare S.B., Sachdev R.K., Yuschekoff V.N., Birkett N.C.,
RA Williams L.R., Satyagal V.N., Tung W., Bosselman R.A., Mendiaz E.A.,
RA Langley K.E.;
RT "Identification, purification, and biological characterization of
RT hematopoietic stem cell factor from buffalo rat liver conditioned
RT medium."
RL Cell 63:195-201(1990).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
CC PROBABLY INTERLEUKINS.
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SECRETED SOLUBLE FORM.
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.

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CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).

DR EMBL: M59966; AAA42117.1; -
DR PIR: B35974; B35974.
DR PIR: A35973; A35973.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF, 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25
FT CHAIN 26 >201
FT MOD.RES 26 26
FT DISULFID 29 114
FT DISULFID 68 163
FT CARBOHYD 90 90
FT CARBOHYD 145 145
FT CARBOHYD 167 167
FT CARBOHYD 168 168
FT CARBOHYD 180 180
FT CARBOHYD 195 195
FT NON_TER 201 201
SQ SEQUENCE 201 AA; 22537 MW; 188868C1DA4F271B CRC64;
KIT LIGAND.
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .) (PARTIAL).
O-LINKED (PROBABLE).
O-LINKED (PROBABLE).
O-LINKED (PROBABLE).
N-LINKED (GLCNAC. . .) (PARTIAL).

Query Match 80.8%; Score 857; DB 1; Length 201;
Best Local Similarity 82.6%; Pred. No. 3e-60;
Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

OY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNVTNNKDVTKLVANLPKDWITLKYVG 60
DB 1 MKKTQWITTCIYLQLLFNPLVKTGICRNVTNNKDVTKLVANLPKDWITLKYVG 60
OY 61 MDVLPSCHEWISVMVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
DB 61 MDVLPSCHEWISVMVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
OY 121 KDLKSKFSKSPERLFTPEEFRIENRSDAFKDFVVASNSDCVVSSTLSPKDSRVSV 180
DB 121 KDLKSKFSKSPERLFTPEEFRIENRSDAFKDFVVASNSDCVVSSTLSPKDSRVSV 180
OY 181 KPFMLPVAASLRNDSSSSN 201
[1]

DB 181 KPEMLPVAASLRNDSSSN 201

RESULT 5
SCF_MOUSE STANDARD: PRT: 273 AA.

AC SCF_MOUSE
AC P20826:
DT 01-FEB-1991 (Rel. 17, last sequence update)
DT 01-MAY-1991 (Rel. 18, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Hematopoietic growth factor KL) (KL-1 protein) (Steel factor).
GN KITLG OR KITL OR MGF OR SL OR SLF.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCB6F1;
RX MEDLINE=91004223; PubMed=1698558;
RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J., Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D., Williams D.E.;
RT "Molecular cloning of mast cell growth factor, a hematopoietin that is active in both membrane bound and soluble forms.";
RL Cell 63:235-243(1990).
RN

[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT "Differential expression and processing of two cell associated forms of the Kit-ligand: KL-1 and KL-2.";
RL Mol. Biol. Cell 3:349-362(1992).
RN

[3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=MCB6F1;
RX MEDLINE=91160046; PubMed=1705866;
RA Flanagan J.G., Chan D.C., Leder P.;
RT "Transmembrane form of the Kit ligand growth factor is determined by alternative splicing and is missing in the Sld mutant.";
RL Cell 64:1025-1035(1991).
RN

[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93012940; PubMed=1383087;
RA Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A., Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.;
RT "Developmental abnormalities in Steel17H mice result from a splicing defect in the steel factor cytoplasmic tail.";
RL Genes Dev. 6:1832-1842(1992).
RN

[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=97002551; PubMed=8849898;
RA Bedell M.A., Copeland N.G., Jenkins N.A.;
RT "Multiple pathways for Steel regulation suggested by genomic and sequence analysis of the murine Steel gene.";
RL Genetics 142:927-934(1996).
RN

[6]
RP SEQUENCE FROM N.A.
RC STRAIN=(102/ELXC3H/EL)F1; TISSUE=Brain;
RX Graw J.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN

[7]
RP SEQUENCE OF 1-270 FROM N.A., AND SEQUENCE OF 26-65.
RX MEDLINE=91004221; PubMed=1698557;
RA Huang E., Nocka K., Beier D.R., Chu T.Y., Buck J., Lahm H.W., Wellner D., Leder P., Besmer P.;
RT "The hematopoietic growth factor KL is encoded by the Sl locus and is the ligand of the c-kit receptor, the gene product of the W locus.";
RL Cell 63:225-233(1990).

[8]
RP SEQUENCE OF 1-201 FROM N.A.
RX MEDLINE=91004220; PubMed=1698556;
RA Zeebo K.M., Williams D.A., Geisler E.N., Broudy V.C., Martin F.H., Atkins H.L., Hsu R.-Y., Birckett N.C., Okino K.H., Murock D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeshi T., Catnach B.M., Galli S.J., Sugas S.V.;
RT "Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for the c-kit tyrosine kinase receptor.";
RL Cell 63:213-224(1990).
RN

[9]
RP SEQUENCE OF 26-53.
RX MEDLINE=91004216; PubMed=1698554;
RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A., Cosman D., Anderson D., Lyman S.D., Williams D.E.;
RT "Mast cell growth factor maps near the steel locus on mouse chromosome 10 and is deleted in a number of steel alleles.";
RL Cell 63:175-183(1990).
RN

[10]
RP PARTIAL SEQUENCE OF 26-78.
RX MEDLINE=91004215; PubMed=1698553;
RA Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K., March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S., Burgess G.S., Cosman D., Lyman S.D.;
RT "Identification of a ligand for the c-kit proto-oncogene.";
RL Cell 63:167-174(1990).
RN

-1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.
CC
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.
CC
CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVELY SPLICED FORMS DIFFERING BY THE PRESENCE OR ABSENCE OF EXON 6 HAVE BEEN OBSERVED AND OCCUR IN VARYING RATIOS IN DIFFERENT TISSUES.
CC
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC
CC -1- PIM: THE LONG FORM APPEARS TO CONTAIN A PROTEOLYTIC CLEAVAGE SITE ENCODED BY EXON 6 SUCH THAT THE ACTIVE REGION OF THE EXTRACELLULAR DOMAIN IS RELEASED FROM THE MEMBRANE IN A SOLUBLE FORM.
CC
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC

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CC
CC EMBL: M59915; AAA40095.1; -;
CC EMBL: M57647; AAA39538.1; -;
CC EMBL: X68989; CAA48778.1; -;
CC EMBL: U44724; -; NOT ANNOTATED_CDS.
CC EMBL: U44725; AAC52447.1; -;
CC EMBL: X9581; CAA64667.1; -;
CC EMBL: S40364; AAB22554.2; -;
CC EMBL: M59912; AAA39539.1; -;
CC PIR: A35971; A35971.
CC PIR: A35972; A35972.
CC PIR: A35975; A35975.
CC PIR: A35976; A35976.
CC PIR: A35977; A35977.
CC PIR: A43751; A43751.
CC PIR: B35971; B35971.
CC MGD: MGI:96974; Kitl.
CC InterPro: IPR003452; SCF.
CC Pfam: PF02404; SCF, 1.
CC Growth factor; Glycoprotein; Transmembrane; Signal;
CC Alternative splicing; Cell adhesion.
CC SIGNAL 1 25
CC CHAIN 26 273 KIT LIGAND.

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FT DOMAIN 26 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 237 POTENTIAL.
FT DOMAIN 238 273 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 114 BY SIMILARITY.
FT DISULFID 68 163 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 175 202 MISSING (IN SOLUBLE ISOFORM).
FT VARIANT 207 207 A -> S.
FT CONFLICT 215 215 W -> L (IN REF. 2).
SQ SEQUENCE 273 AA; 30645 MW; A7FC89B592A7967 CRC64;

Query Match
Best Local Similarity 80.6%; Score 855; DB 1; Length 273;
Matches 167; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPVLTGEGICRNRVNNKVDYTKLVANLPKDYMTLKYPG 60
DB 1 MKKTQWILTCIYLQLLFNPVLTGEGICRNRVNNKVDYTKLVANLPKDYMTLKYPG 60
QY 61 MDVLPSCWISPMVQVLSLTLDLKFSNISGLSNYSIIDKLVIYDDVLECYKENS 120
DB 61 MDVLPSCWISPMVQVLSLTLDLKFSNISGLSNYSIIDKLVIYDDVLECYKENS 120
QY 121 KDLSKFSKPEPRLEFPEEFRIIPNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRYST 180
DB 121 KNIKESKRPETSFTEEFESIFNRSIDAFKDFVVASSETSDCVSSTLSPEKDSRYST 180
QY 181 KPEMLPVAASSLRNDSSSSNSK 203
DB 181 KPEMLPVAASSLRNDSSSSNSK 203

RESULT 6
SCF_CHICK STANDARD; PRT; 287 AA.
ID SCF_CHICK
AC 009108;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE kit ligand precursor (C-Kit ligand) (stem cell factor) (SCF) (Mast
DE cell growth factor) (MGF).
GN KITLG.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9373244; PubMed=7684722;
RA Zhou J., Ohtaki M., Sakurai M.;
RT "Sequence of a cDNA encoding chicken stem cell factor.";
RL Gene 127:269-270(1993).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
CC AUGMENT THE PROLIFERATION OF BOTH MARELOID AND LYMPHOID
CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CC CELL-CELL ADHESION. ACTS SYNGEGISTICALLY WITH OTHER CYTOKINES,
CC PROBABLY INTERLEUKINS.
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SECRETED SOLUBLE FORM.
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D13516; BAA0273.1; -.
CC PIR: J0637; J0637.
CC InterPro: IPR003452; SCF.
CC Pfam: PF02404; SCF.
CC Growth factor; Glycoprotein; Transmembrane; signal; Cell adhesion.
KW SIGNAL 1 25
FT CHAIN 26 287 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 26 225 KIT LIGAND.
FT TRANSMEM 226 246 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 247 287 CYTOPLASMIC (POTENTIAL).
FT DISULFID 29 117 BY SIMILARITY.
FT DISULFID 68 167 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 287 AA; 32328 MW; 6AE856ADCI52578 CRC64;

Query Match
Best Local Similarity 53.0%; Score 562.5; DB 1; Length 287;
Matches 113; Conservative 36; Mismatches 53; Indels 5; Gaps 3;

QY 1 MKKTQWILTCIYLQLLFNPVLTGEGICRNRVNNKVDYTKLVANLPKDYMTLKYPG 60
DB 1 MKKTQWILTCIYLQLLFNPVLTGEGICRNRVNNKVDYTKLVANLPKDYMTLKYPG 60
QY 61 MDVLPSCWISPMVQVLSLTLDLKFSNT---SEGLSNYSIIDKLVIYDDVLECYKE 117
DB 61 MDVLPSCWISPMVQVLSLTLDLKFSNT---SEGLSNYSIIDKLVIYDDVLECYKE 117
QY 118 NSSKD-LKSKFSKPEPRLEFPEEFRIIPNRSIDAFKDFVVASSETSDCVSSTLSPEKDS 175
DB 121 DNKDFIKENGLHYEDREFIPENFRLEPNSTIEYKEFADSLDNDCMPSTVEPENDS 180
QY 176 RVSATKPEMLPVAASSLRNDSSSSNS 202
DB 181 RVSATKPEMLPVAASSLRNDSSSSNS 202

RESULT 7
SCA4_RICE STANDARD; PRT; 961 AA.
ID SCA4_RICE
AC Q9AJ37;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
DE (Protein PS 120) (Fragment).
GN SCA4 OR P.
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=42862;
RN [1]
RP SEQUENCE FROM N.A.
RX Sekeyova Z., Roux V., Raoult D.;
RT "Phylogenetic analysis of Rickettsia spp. by comparing the sequence of
RT gene D coding for an intracytoplasmic protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF196973; AAK31304.1; -.

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KW Antigen. 1 1
 FT NON_TER 981 981
 SQ SEQUENCE 981 AA; 107514 MW; 7F18F421E2C262E1 CRC64;

Query Match 9.6%; Score 102; DB 1; Length 981;
 Best Local Similarity 23.8%; Pred. No. 1.6;
 Matches 62; Conservative 34; Mismatches 87; Indels 78; Gaps 14;

OY 19 FNPVKTGEGICRNRYNNVND-----VTKLVANLPKDYMITLKVPGM-DV 63
 DB 628 FNTAKTAPAI--QVNTTKVLDSPKAEKGTETISIRKVAESPLNQDKADYKKGGEA 685
 OY 64 LPSH-----CWISEMVQVSDSLTDLIDK-----FSNISEGLNSTY----- 100
 DB 686 IASHKTMAPTEKISTIESEVGEVASEITDLEDKKIMTKGLVEGYEKGANPEITSEKTKA 745
 OY 101 ----IDKLVNIVD-----VCEVKE-----NSSKDKK-SFKSPPEPLFTPEEPRIE 144
 DB 746 VSRGIDKSTAIPEQKALKDANEAALDRETQNLTEGIKRONLGEPR-----DDIYNKA 801
 OY 145 NRSIDAFKDFV-----ASETSDCVYSSSTLSPEND-SRVSATK-----PFMLPP 187
 DB 802 QDVADALKNVITPVLDAPKEKREVESEE-VYKKTSTILNDISKLAIEKVNFRAMLSPD 860
 OY 188 VAASSLRNDSSSSNKITYLI 208
 DB 861 GNLKTELEKKAESTKKVVELY 881

RESULT 8

COPG_YEAST STANDARD: PRT: 935 AA.

AC P32074;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coatomer gamma subunit (Gamma-coat protein) (Gamma-COP).
 GN SEC21 OR YNL287W OR N0543.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93096049; PubMed=1461285;
 RA Hosobuchi M.M., Kreis T., Schekman R.;
 RT "SEC21 is a gene required for ER to Golgi protein transport that
 RT encodes a subunit of a yeast coatomer.";
 RL Nature 360:603-605(1992).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Messenguy F., Dubois E., Vierendeels F., Scherrens B., Pierard A.,
 RA Glansdorff N.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
 CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
 CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
 CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
 CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
 CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
 CC TRANSPORT OF DILYSINE-TAGGED PROTEINS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
 CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
 CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
 CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE COPG FAMILY.

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DR EMBL; M59708; AAA34598.1; -
 DR EMBL; 271563; CA96204.1; -
 DR PIR; A33151; A33151.
 DR PIR; S28915; S28915.
 DR SGD; S0005231; SEC21.
 DR InterPro; IPR002553; Adaptin.N.
 DR Pfam; PF01602; Adaptin.N.1.
 KW Transport; Protein transport; Golgi stack; Membrane.
 FT CONFLICT 353 353 D -> N (IN REF. 1).
 SQ SEQUENCE 935 AA; 104830 MW; 99DC7D737DAE761 CRC64;

Query Match 8.7%; Score 92; DB 1; Length 935;
 Best Local Similarity 22.4%; Pred. No. 9.1;
 Matches 51; Conservative 40; Mismatches 79; Indels 58; Gaps 11;

OY 20 NPLVKTGEGICRNRYNNVNDV-TLVANLPKDYMITLKVPGM-----DVLPSHCWIS- 72
 DB 149 HPSISAAALCTSYHLLPISEVTIRPTNETQEAVIDLKQFPNQHNSERYPNSTYISQYH 208
 OY 73 ----MVQLSD-----SLTDLDFKFSNISGLSNYSIIDKLVNIVDLY----- 112
 DB 209 ALGLVQLKTKDKMALKLVHRHSE-NNSMKNQALKVELVKLVNLDIYNDPLFSQFRLP 267
 OY 113 -----ECYKENSCKDKSFKSPPEPLTTPPEEFIFNRSIDAFKDFVVASETDC 163
 DB 268 LSDMLSNKRESVQLEFAK-LITSFAFRNSRLVAPE---LYAAISALQSLTIVPRVSR 322
 OY 164 VVS-----STLSPKDSRVSVTKPFMLPVAASSLRNDSSSSNSKY 204
 DB 323 FAALRLILNRISWVSPK-----IYVCNPEL-----ESLINDSRNISTY 361

RESULT 9

MYSC_HUMAN STANDARD: PRT: 1742 AA.

AC Q9N0X4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin Vc (Myosin 5C).
 GN MYO5C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rodriguez O.C., Cheney R.E.;
 RT "Cloning and characterization of myosin Vc, a third member of the
 RT myosin V family in vertebrates."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 6 IO DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 DILUTE DOMAIN.

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DR EMBL; AF272390; AAF78783.1; -
 DR InterPro; IPR002710; DIL.
 DR InterPro; IPR000048; IO.
 DR InterPro; IPR001609; myosin_head.

DR Pfam; PF01843; DIL; 1.
 DR Pfam; PF00063; myosin_head; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR Prodom; PD000355; myosin_head; 1.
 DR Prodom; PD003376; DIL; 1.
 DR SMART; SM00015; IQ; 5.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS50096; IQ; 4.
 KW Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
 KW Coiled coil; Polymorphism.
 FT DOMAIN 1 755 MYOSIN HEAD-LIKE.
 FT DOMAIN 756 779 IQ 1.
 FT DOMAIN 780 806 IQ 2.
 FT DOMAIN 807 829 IQ 3.
 FT DOMAIN 830 854 IQ 4.
 FT DOMAIN 855 884 IQ 5.
 FT DOMAIN 884 1351 COILED COIL (POTENTIAL).
 FT DOMAIN 1574 1679 DIUTTE.
 FT VARIANT 522 522 P -> L.
 FT VARIANT 634 634 /FTID-VAR_010646.
 FT VARIANT 634 634 L -> S.
 FT SEQUENCE 1742 AA; 202793 MW; 25DD3082A7EB5AAB CRC64;

Query Match 8.5%; Score 90.5; DB 1; Length 1742;
 Best Local Similarity 23.4%; Pred. No. 25;
 Matches 43; Conservative 33; Mismatches 73; Indels 35; Gaps 9;

QY 38 KDTKLVANPKRYM--TLTKVPGMDVPSHCWISENVQISLTD--LIDKFSN-- 90
 DB 1369 EDAKLIQNLIDLPKRGVAVNIPG---LPAH--ILFMCVRADSLDANMLKSLMNST 1423
 QY 91 -----ISEGLSNYSIIDKLVNIVDLVECVKENSXDLKSKSFKEPRL-----FTPE 138
 DB 1424 INGIKQVKEHLEDFEMLSTWLSNTHFLNCLKQYSGEPEFKHNSPQONKKNCLNFDLS 1483
 QY 139 EFRIRNR-SIDAFKFFVASETS--DCVYSTLSPEKDSRVSVTKPFMLPVAASLRLN 195
 DB 1484 EYRQILSDVAIRIHFQIIMEKNIQPIIVPGMLEYSLQGISGLKPF-----TGFRK 1535
 QY 196 DSSS 199
 DB 1536 RSSS 1539

RESULT 10
 PTP3_DICDI STANDARD; PRT; 989 AA.
 ID PTP3_DICDI
 AC P54637;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase 3)
 GN (PTPC1 OR PTP3) AND (PTPC2 OR PTP3).
 OS Dictyostelium discoideum (slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RX MEDLINE=96189126; PubMed=8628311;
 RA Gamber M., Howard P.K., Hunter T., Firtel R.A.;
 RT Multiple roles of the novel protein tyrosine phosphatase PTP3 during Dictyostelium growth and development.;
 RL Mol. Cell. Biol. 16:2431-2444(1996).
 CC -1- FUNCTION: SEEMS TO DEPHOSPHORYLATE A PROTEIN OF 130 kDa (p130).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: IN THE ANTERIOR-LIKE AND PRESTALK CELL TYPES.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT MODERATE LEVELS DURING GROWTH

CC AND DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: U38197; AAC47041.1; -.
 CC HSSP; Q06124; 2SHR.
 DR DictyDB; DD01111; PTPC1.
 DR DictyDB; DD07272; PTPC2.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_prot_phptase.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYHPHTASE.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolase.
 FT ACT_SITE 649 649 BY SIMILARITY.
 FT DOMAIN 460 716 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 64 71 POLY-ASN.
 FT DOMAIN 109 118 POLY-ASN.
 FT DOMAIN 137 190 POLY-ASN.
 FT DOMAIN 249 257 POLY-SER.
 FT DOMAIN 258 265 POLY-SER.
 FT DOMAIN 286 289 POLY-THR.
 FT DOMAIN 366 371 POLY-ASN.
 FT DOMAIN 787 790 POLY-SER.
 FT DOMAIN 834 839 POLY-GLN.
 FT DOMAIN 883 892 POLY-GLN.
 FT DOMAIN 906 914 POLY-ASN.
 FT DOMAIN 943 963 POLY-ASN.
 FT SEQUENCE 989 AA; 109995 MW; 9371105AF80974AF CRC64;

Query Match 8.4%; Score 89; DB 1; Length 989;
 Best Local Similarity 19.5%; Pred. No. 17;
 Matches 33; Conservative 37; Mismatches 61; Indels 38; Gaps 6;

QY 71 SEMVQUSDLTDLDFKSNISEGLSNYSIIDKLVN-IVDLVECVKENSXDLKSKFK- 128
 DB 677 SQNMISIKDSVLELRQRGHWOTLDQYIFLFKVINVDLDM-GIRSLSPSKRRCEM 734
 QY 129 ---SPEPRL-----FTPEEFRIFNNSIDAFKFFVASETSDCV----- 164
 DB 735 IKSTPMPLDISIPPLTFPKDFOSSISPTMIASLTITQWTLKFPPOQDDNPF 794
 QY 165 ---VSTLSPEKDSRVSVTK-----PFMLPVAASLNDSSNSK 203
 DB 795 SKSKIKTISPPLNSTINISIRKQGFQHPFQIQQLDNLQDQDQDQSSQ 843

RESULT 11
 UN13_CAEEL STANDARD; PRT; 1815 AA.
 ID UN13_CAEEL
 AC P27715;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Phorbol ester/diacylglycerol-binding protein unc-13.
 GN UNC-13.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae.
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

Db 141 --CSYINRSCRDWISQVAFSGSVQ-KTGKPVKFIWEFRTRDWDVFIYFVRKGERAI 197
 QY 165 V---SSTLSEKDSRVSTKPEMLPVAAS-----SLNDSSSSNSK 203
 Db 198 YVAGEGKIPSNDECYRWTRREFKREMWSSDCTDYIECEQOBHKISRSDAGSSNGR 255

RESULT 13
 CAP_MEDSA STANDARD: PRT: 966 AA.
 AC 002735:
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCASE).
 GN PEPC.
 OS Medicago sativa (Alfalfa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 ON NCBI_TaxID=3879;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93043034; PubMed=1421147;
 RA Patrino S.M., Vance C.P., Miller S.S., Gantt J.S.;
 RT "Alfalfa root nodule phosphoenolpyruvate carboxylase:
 RT characterization of the cDNA and expression in effective and
 RT plant Mol. Biol. 20:437-450(1992).
 RL (2)
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. SARANAC;
 RA Patrino S.M., Gantt J.S.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TO FORM OXALOACETATE, A FOUR-CARBON DICARBOXYLIC ACID
 CC SOURCE FOR THE TRICARBOXYLIC ACID CYCLE.
 CC -1- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
 CC Phosphoenolpyruvate + CO(2).
 CC -1- ENZYME REGULATION: BY LIGHT-REVERSIBLE PHOSPHORYLATION.
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M83086; AAB46618.1; -;
 DR EMBL; L39371; AAB41903.1; -;
 DR PIR; S26235; S26235.
 DR HSSP; P00864; IFIY.
 DR InterPro: IPR001440; PEPCase.
 DR Pfam; PF00331; PEPCase; 1.
 DR PRINTS; PR00150; PEPCARBLASE.
 DR PROSITE; PS00393; PEPCASE_2; 1.
 DR PROSITE; PS00781; PEPCASE_1; 1.
 KW Lyase; Carbon dioxide fixation; Allosteric enzyme;
 KW Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.
 FT MOD_RES 10
 FT ACT_SITE 171
 FT ACT_SITE 601
 FT ACT_SITE 601
 FT SEQUENCE 966 AA; 110889 MW; 5828EA10C2C41DD7 CRC64;

Query Match 8.28; Score 87.5; DB 1; Length 966;
 Best Local Similarity 24.78; Pred. No. 21;
 Matches 39; Conservative 31; Mismatches 59; Indels 29; Gaps 8;

QY 2 KKTQVITLCITYLDLLFNP-LVKTEGICRRNRYNNKVDYTKLVANPKD---YMTLK 56
 Db 479 EKROEMLSELIGKRPLFEGPDLPTDTEL-----RDVLDFFRYIAELPSPNFGAIIISMA 532
 QY 57 YVP---GMDVLPSPHWISE--MVVQSDSLTLDLFNSNSEGLSYSLIDKLVNYVD 110
 Db 533 TAPSDVLAVELLORECKRYRNLRYVPLFEKLDL-----ESAPALARLFSIDWYINRIGD 568

QY 111 LVECV--KENSCKDKR-----SEKSPERLFTPEEP 140
 Db 589 KOEWMIGYSDGSKDAGRFAAMQLYKAOEDLIKVAQKE 626

RESULT 14
 ZAA_CAEEL STANDARD: PRT: 664 AA.
 ID ZAA_CAEEL
 AC 009543;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable protein phosphatase PP2A regulatory subunit (Protein
 DE phosphatase PP2A regulatory subunit A).
 GN P48B.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Kirsten J.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE PP2A SUBUNIT OF PROTEIN PHOSPHATASE 2A SERVES AS A
 CC SCAPOLDING MOLECULE TO COORDINATE THE ASSEMBLY OF THE CATALYTIC
 CC SUBUNIT AND A VARIABLE REGULATORY B SUBUNIT (BY SIMILARITY).
 CC -1- SUBUNIT: PP2A EXISTS IN SEVERAL TRIMERIC FORMS, ALL OF WHICH
 CC CONSIST OF A CORE COMPOSED OF A CATALYTIC SUBUNIT ASSOCIATED WITH
 CC A 65 kDa REGULATORY SUBUNIT (PP65) (SUBUNIT A), THE CORE COMPLEX
 CC ASSOCIATES WITH A THIRD, VARIABLE SUBUNIT (SUBUNIT B), WHICH
 CC CONFERES DISTINCT PROPERTIES TO THE Holoenzyme (BY SIMILARITY).
 CC -1- DOMAIN: EACH HEAT REPEAT APPEARS TO CONSIST OF TWO ALPHA HELICES
 CC JOINED BY A HYDROPHILIC REGION, THE INTRAREPEAT LOOP. THE REPEAT
 CC UNITS MAY BE ARRANGED LATERALLY TO FORM A ROD-LIKE STRUCTURE.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT A
 CC FAMILY.
 CC -1- SIMILARITY: CONTAINS 15 HEAT REPEATS.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U23514; AAC64541.1; -;
 DR HSSP; P30153; LB3U.
 DR WormPep; P48B.5; CE01957.
 DR InterPro: IPR000357; HEAT_repeat.
 DR Pfam; PF02985; HEAT_14.
 DR PROSITE; PS50077; HEAT_REPEAT; 8.
 KW Hypothetical protein; Repeat.
 FT REPEAT 84
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Query Match 8.2%; Score 87; DB 1; Length 664;
 Best Local Similarity 23.2%; Pred. No. 15;
 Matches 35; Conservative 32; Mismatches 50; Indels 34; Gaps 6;

Query 12 IYIQLLNFNVLT-----GICRNTNNKDYTKLVANLPKDYMTLTKYVPG 60
 Db 495 VRLAIVGFEMPLASQLGQEFDEKLLPLCLNLTLDHVFSTREASTLTKKE--LTQKF--- 549
 QY 61 MDVLPSCHWISEWVGLSDSL--TDLTDK-----FSNISGLSNYSIIDLKLVNIVDDL 111
 Db 550 -----GGQMASTNIVPKMKQLQKDTNVLQRMTCLEFCINTLSEAMTQEQILKEIMPIVKDL 604
 QY 112 VE---CVKENSXKDKLKKSFSPPEPLTPE 138
 Db 605 VEDDVVNVRFNAKSLKRIKGNLTPTLTISE 635

RESULT 15
 BRO1_YEAST STANDARD; PRT; 844 AA.

AC P48582; Q02823;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE BRO1 protein.
 GN BRO1 OR YPL084W OR LPP2.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;

Sequence from N.A.
 MEDLINE=96220442; PubMed=8649366;
 RA Nickas M.E., Yaffe M.P.;
 RT "BRO1, a novel gene that interacts with components of the
 RT PKC β -mitogen-activated protein kinase pathway in Saccharomyces
 RT cerevisiae." Mol. Cell. Biol. 16:2585-2593(1996).

Sequence from N.A.
 Hall J., Ahmed A., Bussey H., Fortin N., Friesen J.D., Storms R.K.,
 RA Vo D.H., Wang Y., Winnett E.;
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INTERACTS WITH COMPONENTS OF THE PKC1-MAP KINASE
 CC PATHWAY.
 CC -!- SIMILARITY: SOME, TO C.ELEGANS R10E12.1.

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 or send an email to license@sib-sib.ch).

EMBL; U37364; AAB07790.1; -;
 EMBL; U41849; AAB68255.1; -;
 DR SGD; S0006005; BRO1.
 DR InterPro; IPR004328; BRO1.
 Pfam; PF03097; BRO1; 1.
 FT CONFLICT 359 359 Y -> C (IN REF. 2).
 FT SEQUENCE 844 AA; 97335 MW; 344905ADB845FFB CRC64;

Query Match 8.2%; Score 86.5; DB 1; Length 844;
 Best Local Similarity 26.3%; Pred. No. 22;
 Matches 47; Conservative 27; Mismatches 74; Indels 31; Gaps 9;

Query 30 RNRVTNNKDYTKLVANLPKDYMTLTKYVPGMDY---LPSCHWISEWVGLSDSLDLD 86
 Db 578 RDEINND--DITKLLINKGKSDVELKDLDFEVELEKEPEPSTRLEATYKQSSMIDDKA 635
 QY 87 KFSNISGLSNV-----SIIDLKLVNIVDLYECYKENS--SKDLKSKSFSPPEPLTFT 136
 Db 636 KLDETFH--LSNFKDKSSGGEKFLDRKNFPKLOEAVKSFISFASDLPKGI----- 685
 QY 137 PEEFP-RIFNRSIDAFKDFVVASETSDCVSSTLS--PEKDSRVSVT-KPPMLPPVAAS 191
 Db 686 --EFYDSLFNMSRDLAERVRAKQTEDSTANSAPAPLPLPILDSKASVVGPPLLPQKSA 742

Search completed: August 18, 2002, 13:02:05
 Job time: 50 sec

Sun Aug 18 14:09:02 2002

us-09-604-325a-46.rsp

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 13:01:15 ; Search time 114.11 seconds
(without alignments)
315.336 Million cell updates/sec

Title: US-09-604-325A-46
Perfect score: 1061
Sequence: 1 MKKTQWTILTCIYLQLLFN.....AASLRNDSSSSNKYIYLI 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacterioplasmid:*
17: SP-archaeplastid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	908.5	85.6	274	6	P79169 felis silve
2	889.5	83.8	267	6	P79368 ovis aries
3	886.5	83.6	274	6	Q28132 bos taurus
4	885.5	83.5	274	6	Q95M19 capra hircu
5	883.5	83.3	261	6	Q95MD2 equus caball
6	877	82.7	245	4	Q9UOK7 equus caball
7	861	81.1	273	11	Q9QWZ4 ratu
8	859.5	81.0	274	6	Q95N18 mustela vis
9	855	80.6	208	11	Q64384 mus musculu
10	855	80.6	273	11	Q921N5 mus musculu
11	848	79.9	273	11	Q62524 mus musculu
12	847	79.8	273	11	Q62765 mus musculu
13	831.5	78.4	256	6	Q62765 mus musculu
14	725.5	68.0	260	6	Q95MNS mustela vis
15	721	68.0	245	11	Q922E7 ratu
16	716	67.5	245	11	Q64222 mus sp. c-k

17	570.5	53.8	287	13	Q90314 coturnix co
18	509	48.0	123	11	Q61854 mus musculu
19	479.5	45.2	253	13	Q90315 coturnix co
20	401.5	37.8	96	6	Q95M88 equus caball
21	327	30.8	271	13	Q9YGP2 ambystoma m
22	214.5	20.2	51	6	Q9N1Y5 equus caball
23	100	9.4	3072	12	Q92645 clover yell
24	97.5	9.2	1490	5	Q19545 ureaplasma
25	97	9.1	1447	16	Q9PQJ8 ureaplasma
26	96.5	9.1	1498	3	Q9P884 ureaplasma
27	96.5	9.1	1498	3	Q9P884 ureaplasma
28	94.5	8.9	576	11	Q62970 emeritella
29	94	8.9	1238	12	Q9EMP3 ratu
30	94	8.9	1813	5	Q17665 emeritella
31	93.5	8.8	579	11	Q99KW2 caenorhabdi
32	92.5	8.7	164	16	P71021 bacillus su
33	92.5	8.7	512	16	Q9CGA7 bacillus su
34	92	8.6	188	5	Q9VRK2 drosophila
35	91.5	8.6	976	2	Q54222 staphylococ
36	91	8.6	317	5	Q9V172 drosophila
37	91	8.6	422	12	Q911I4 white spot
38	91	8.6	1107	3	Q12271 saccharomyc
39	90.5	8.5	254	11	Q9J1I6 methanococ
40	90.5	8.5	616	17	Q26384 methanococ
41	90	8.5	937	10	Q9M1L4 arabidopsis
42	90	8.5	1219	12	Q911B1 white spot
43	90	8.5	1501	3	Q96VU9 botrytis ci
44	88.5	8.3	228	2	Q9XC73 salmonella
45	88.5	8.3	941	10	Q9S1N0 arabidopsis

ALIGNMENTS

RESULT 1
ID P79169 PRELIMINARY; PRT; 274 AA.
AC P79169;
DT 01-MAY-1997 (TREMURel. 03, Created)
DT 01-MAY-1997 (TREMURel. 03, Last sequence update)
DT 01-DEC-2001 (TREMURel. 19, Last annotation update)
DE STEM CELL FACTOR.
GN SCF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97069946; PubMed=8912926;
RX Dunham S.P., Orlowski D.E.;
RT "The cloning and sequencing of cDNAs encoding two isoforms of feline
RT stem cell factor."
RL DNA Seq. 6:233-237(1996).
DR EMBL; D50833; BAA09445.1; -
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
SO SEQUENCE 274 AA; 30987 MM; C5B78DB4791237BE CRC64;

Query Match 85.6%; Score 908.5; DB 6; Length 274;
Best local similarity 88.2%; Pred. No. 2e-68;
Matches 180; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

QY 1 MKKTQWTILTCIYLQLLFNPKYKTEGICNRRVTNNVKKVTKLVANLPKDYMTTKLYVG 60
DB 1 MKKTQWTILTCIYLQLLFNPKYKTEGICNRRVTNNVKKVTKLVANLPKDYMTTKLYVG 60
QY 61 MDVLPSCWISSENVVDSLDLDFKFSNISGLSNYSIIKLVIVVDLVCYKENS 120
DB 61 MDVLPSCWISSENVVDSLDLDFKFSNISGLSNYSIIKLVIVVDLVCYKENS 120
QY 121 KDLKSKSPKSPKPLPTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSPKSDRSV 179

Db 121 ENVKSSSPRLFTPEEFRIKRSIDAFKLEWASTSECVSTLSPKDSRVSV 180
 Oy 180 TKPFMLPPVAASLRNDSSSSNRK 203
 Db 181 TKPFMLPPVAASLRNDSSSSNRK 204

RESULT 2
 P79368 PRELIMINARY; PRT; 267 AA.
 ID P79368: 028591;
 AC 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE STEM CELL FACTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RX MEDLINE=96413880; PubMed=8662240;
 RA Tisdall D.J., Quirke L.D., Galloway S.M.;
 RT "Ovine stem cell factor gene is located within a syntenic group on
 RT chromosome 3 conserved across mammalian species."
 RL Mamm. Genome 7:472-473(1996).
 RN [12]
 RP SEQUENCE OF 8-267 FROM N.A.
 RC TISSUE=OVARIAN FOLLICLE;
 RA Tisdall D.J., Quirke L.D.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE OF 1-202 FROM N.A.
 RA McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haly D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U89874; ABA49491.1; -;
 DR EMBL: Z50743; CA90620.1; -;
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 FT NON_TER 267
 SQ SEQUENCE 267 AA; 30148 MW; 9D9D959E4B9C841 CRC64;

Query Match 83.8%; Score 889.5; DB 6; Length 267;
 Best Local Similarity 85.8%; Pred. No. 7.7e-67;
 Matches 175; Conservative 15; Mismatches 13; Indels 1; Gaps 1;

Oy 1 MKKTQWITTCYIQLLLFNPLVTEGICRNRTNNKVDVTKLVANLPKDYMITLKYVG 60
 Db 1 MKKTQWITTCYIQLLLFNPLVHTOGICRNRTVDVTKLVANLPKDYMITLKYVG 60
 Oy 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISGLSNYSIIDKLVNIYVDLVECKEHSF 120
 Oy 121 KDILKSKSPERLFTPEEFRIKRSIDAFKDF-VVASSETSCVYSTLSPKDSRVSV 179
 Db 121 ENVKSSSPRLFTPEEFRIKRSIDAFKDFLEIVASTMSECVISTSPKDSRVSV 180
 Oy 180 TKPFMLPPVAASLRNDSSSSNRK 203
 Db 181 TKPFMLPPVAASLRNDSSSSNRK 204

RESULT 3
 028132 PRELIMINARY; PRT; 274 AA.
 AC 028132:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE STEM CELL FACTOR LONGER ISOFORM.
 GN SCF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RX MEDLINE=94339176; PubMed=7520283;
 RA Zhou J., Hakono H., Ohtaki M., Kubota T., Sakurai M.;
 RT "Cloning and characterization of cDNAs encoding two normal isoforms of
 RT bovine stem cell factor."
 RL Blochim. Biophys. Acta 1223:148-150(1994).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RA Kudo T.;
 RT "Bovine counterpart of stem cell factor."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D28934; BAA06061.1; -;
 DR EMBL: AB033716; BAA94808.1; -;
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 SQ SEQUENCE 274 AA; 31014 MW; D6C1DDB77B0CB12B CRC64;

Query Match 83.6%; Score 886.5; DB 6; Length 274;
 Best Local Similarity 85.3%; Pred. No. 1.4e-66;
 Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

Oy 1 MKKTQWITTCYIQLLLFNPLVTEGICRNRTNNKVDVTKLVANLPKDYMITLKYVG 60
 Db 1 MKKTQWITTCYIQLLLFNPLVHTOGICRNRTVDVTKLVANLPKDYMITLKYVG 60
 Oy 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISGLSNYSIIDKLVNIYVDLVECKEHSF 120
 Oy 121 KDILKSKSPERLFTPEEFRIKRSIDAFKDF-VVASSETSCVYSTLSPKDSRVSV 179
 Db 121 ENVKSSSPRLFTPEEFRIKRSIDAFKDFLEIVASTMSECVISTSPKDSRVSV 180
 Oy 180 TKPFMLPPVAASLRNDSSSSNRK 203
 Db 181 TKPFMLPPVAASLRNDSSSSNRK 204

RESULT 4
 095M19 PRELIMINARY; PRT; 274 AA.
 AC 095M19:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE STEM CELL FACTOR.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 NCBI_TaxID=9925;
 RX MEDLINE=94339176; PubMed=7520283;
 RA Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
 RT "Identification of Splicing Isoforms of Caprine Stem Cell Factor
 RT (gSCF) Transcripts and Expression Patterns of the Two Major Isoforms,
 RT gSCF825 and gSCF741, in the Brain and the Skin of Adult and Fetal
 RT Suba Goats, Capra hircus.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB002152; BAB71753.1; -;

SO SEQUENCE 274 AA; 31052 MW; BBE669A509EF65D CRC64;

Query Match 83.5%; Score 885.5; DB 6; Length 274;
Best Local Similarity 85.3%; Pred. No. 1.7e-66;
Matches 174; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYQLLEFNPVLTGEGICRNRVTNNKVDYTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGEGICRNRVTNNKVDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECKENSS 120
QY 121 KDLKFSKSPERLFTPEEFRIFRNSIDAFKDF-VVASETSDCVSSTLSPEKDSRVSY 179
DB 121 ENVKSSKSPERQRTPEKFGIFKSIDAFKDFEIVASTSECVIISSTSPKDSRVSY 180
QY 180 TKPFMLPVAASSLRNDSSSSNSK 203
DB 181 TKPFMLPVAASSLRNDSSSSNSK 204

RESULT 5

Q95MD2 PRELIMINARY; PRT; 261 AA.

AC Q95MD2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MAST CELL GROWTH FACTOR (FRAGMENT).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Bailey E.;
RT "Equus caballus mast cell growth factor (MGF).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF401625; AAK94474.1; -.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 29526 MW; 16A3062105346E4B CRC64;

Query Match 83.3%; Score 883.5; DB 6; Length 261;
Best Local Similarity 86.6%; Pred. No. 2.4e-66;
Matches 174; Conservative 15; Mismatches 11; Indels 1; Gaps 1;

QY 4 TOTWILTCIYQLLEFNPVLTGEGICRNRVTNNKVDYTKLVANLPKDYMITLKYPGMDV 63
DB 1 TOTWILTCIYQLLEFNPVLTGEGICRNRVTNNKVDYTKLVANLPKDYMITLKYPGMDV 60
QY 64 LPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECKENSSKDL 123
DB 61 LPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECKENSSKDL 120
QY 124 KKSFSKSPERLFTPEEFRIFRNSIDAFKDF-VVASETSDCVSSTLSPEKDSRVSYTKP 182
DB 121 KKSFSKSPERLFTPEEFRIFRNSIDAFKDF-VVASETSDCVSSTLSPEKDSRVSYTKP 180
QY 183 FMLPVAASSLRNDSSSSNSK 203
DB 181 FMLPVAASSLRNDSSSSNSK 201

RESULT 6
Q9UOK7 PRELIMINARY; PRT; 245 AA.

AC Q9UOK7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STEM CELL FACTOR (STEM CELL FACTOR ISOFORM 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99160429; PubMed=10049787;
RA Blair H.C., Julian B.A., Gao X., Jordan S.E., Dong S.S.;
RT "Parathyroid hormone-regulated production of stem cell factor in human osteoblasts and osteoblast-like cells.";
RL Biochem. Biophys. Res. Commun. 255:778-784(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Han C., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF119835; AAD22048.1; -.
DR EMBL, AF400437; AAK92486.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 245 AA; 27903 MW; FF87983163A33C36 CRC64;

Query Match 82.7%; Score 877; DB 4; Length 245;
Best Local Similarity 98.3%; Pred. No. 7.7e-66;
Matches 170; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVLTGEGICRNRVTNNKVDYTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGEGICRNRVTNNKVDYTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSLDLDLDFKFSNISSEGLSNYSIIDKLVIYVDLVECKENSS 120
QY 121 KDLKFSKSPERLFTPEEFRIFRNSIDAFKDFVVASETSDCVSSTLSPEK 173
DB 121 KDLKFSKSPERLFTPEEFRIFRNSIDAFKDFVVASETSDCVSSTLSPEK 173

RESULT 7

Q9QWZ4 PRELIMINARY; PRT; 273 AA.

AC Q9QWZ4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STEM CELL FACTOR KL-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Teramoto T., Nagashima M., Thorgelsson S.S.;
RT "Rat-SCF-KL-1.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF071204; AAD02827.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 273 AA; 30712 MW; C0F56527DC93FD27 CRC64;

Query Match 81.1%; Score 861; DB 11; Length 273;
Best Local Similarity 82.3%; Pred. No. 1.9e-64;
Matches 167; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVLTGEGICRNRVTNNKVDYTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVLTGEGICRNRVTNNKVDYTKLVANLPKDYMITLKYPG 60


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Db 121 KNKESKRPETRSFTPEEFISFNSSIDAFKDFMVASDTSOVLSTLGPEDKSRVSVT 180
Qy 181 KPFLPVAASSLRNDSSSSNSK 203
Db 181 KPFLPVAASSLRNDSSSSNSK 203

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RESULT 11
Q62524 PRELIMINARY; PRT; 273 AA.
AC 062524;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE MAST CELL GROWTH FACTOR.
GN KITL OR MGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/E1; TISSUE=BRAIN;
RX MEDLINE=97032534; Pubmed=8875893;
RT "Molecular analysis of two new Steel mutations in mice shows a
RT transversion or an insertion."
RL Mamm. Genome 7:843-846(1996).
DR EMBL: X9322; CAA67698.1; -.
DR MGI: 96974; KitL.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF.
FT VARIANT 193 193 P -> L.
FT VARIANT 207 207 S -> A.
SQ SEQUENCE 273 AA; 30645 MW; B3E9D0B72C734107 CRC64;

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Query Match 79.9%; Score 848; DB 11; Length 273;
Best Local Similarity 81.8%; Pred. No. 2.4e-63;
Matches 166; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MKKTQWITTCIYQLDLFNPVKTGICRNRTNNKDVTKLVANLPKDYMITLKYVPG 60
Db 1 MKKTQWITTCIYQLDLFNPVKTGICGNPVTDVKITLVANLPNDYMITLVYAG 60
Qy 61 MDVLPSCWISSEMVVQSLDSTLTLDFKFSNISEGLSNYSIIDKLVNIYVDLVCEYKENS 120
Db 61 MDVLPSCWISSEMVVQSLDSTLTLDFKFSNISEGLSNYSIIDKLVNIYVDLVCEYKENS 120
Qy 121 KDLKSPKSPRPLFTPEEFIRINRSIDAFKDFVASETSDCVVSSTLSPKDSRYSVT 180
Db 121 KNKESKRPETRSFTPEEFISFNSSIDAFKDFMVASDTSOVLSTLGPEDKSRVSVT 180
Qy 181 KPFLPVAASSLRNDSSSSNSK 203
Db 181 KPFLPVAASSLRNDSSSSNSK 203

RESULT 12
P97332 PRELIMINARY; PRT; 273 AA.
AC P97332;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MAST CELL GROWTH FACTOR.
GN KITL OR MGF S1-3NEU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=102/ELIX3H/EL1;
RX MEDLINE=98025115; Pubmed=9360640;
RA Graw J., Neuhauser-Klaus, Pretsch;
RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
RT gene defines a novel allele at the Steel locus with a weak
RT phenotype."
RL Mutat. Res., Mutat. Res. Genomics 382:75-78(1997).
DR EMBL: Y10287; CAA71329.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF.
FT VARIANT 193 193 P -> L.
FT VARIANT 207 207 S -> A.
SQ SEQUENCE 273 AA; 30618 MW; BC36F17A2C6F90C3 CRC64;

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Query Match 79.8%; Score 847; DB 11; Length 273;
Best Local Similarity 81.8%; Pred. No. 2.9e-63;
Matches 166; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MKKTQWITTCIYQLDLFNPVKTGICRNRTNNKDVTKLVANLPKDYMITLKYVPG 60
Db 1 MKKTQWITTCIYQLDLFNPVKTGICGNPVTDVKITLVANLPNDYMITLVYAG 60
Qy 61 MDVLPSCWISSEMVVQSLDSTLTLDFKFSNISEGLSNYSIIDKLVNIYVDLVCEYKENS 120
Db 61 MDVLPSCWISSEMVVQSLDSTLTLDFKFSNISEGLSNYSIIDKLVNIYVDLVCEYKENS 120
Qy 121 KDLKSPKSPRPLFTPEEFIRINRSIDAFKDFVASETSDCVVSSTLSPKDSRYSVT 180
Db 121 KDLKSPKSPRPLFTPEEFIRINRSIDAFKDFVASETSDCVVSSTLSPKDSRYSVT 180
Qy 181 KPFLPVAASSLRNDSSSSNSK 203
Db 181 KPFLPVAASSLRNDSSSSNSK 203

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RESULT 13
Q62765 PRELIMINARY; PRT; 256 AA.
AC 062765;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE STEM CELL FACTOR HOMOLOG (FRAGMENT).
GN SCF.
OS Equus caballus (horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN.
RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
RT "An Equine sequence homologous to stem cell factor (KIT-ligand).";
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF053498; AAC97076.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF.
FT NON_TER 1 1
FT NON_TER 256 256
SQ SEQUENCE 256 AA; 28933 MW; 9E4876CAEC7B55FF CRC64;

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Query Match 78.4%; Score 831.5; DB 6; Length 256;
Best Local Similarity 86.0%; Pred. No. 5.3e-62;
Matches 166; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

Qy 12 IYQLDLFNPVKTGICRNRTNNKDVTKLVANLPKDYMITLKYVPGMDVLPSCWIS 71
Db 1 IYPLDLFNPVKTGICGNRTVDVKITLVANLPKDYKITLKYVPGMDVLPSCWIS 60

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QY 72 EMVYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECKENSSKDLKSKSPK 131
 DB 61 EMVOHLSVSLTDLDFKFSNISEGLSNYSIIDKLIVDDLVECKENSSKDLKSKSPK 120
 QY 132 PRLFTPEEPFRIRNRSIDAFKDF-VVASSETSDCVSSTISPEKDSVSTTKPFMLPVVA 190
 DB 121 SRLFTPEEPFRIRNRSIDAFKDFEMVYVQSDSLTDLDFKFSNISEGLSNYSIIDKLIVDDLVECKENSSKDLKSKSPK 180
 QY 191 SSLRNDSSSSNSK 203
 DB 181 SSLRNDSSSSNSK 193

RESULT 14

QY 095MN5 PRELIMINARY; PRT: 260 AA.
 AC 095MN5;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE STEM CELL FACTOR SHORT ISOFORM.
 OS Muscula vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mustela.
 OX NCBI_TaxID=9667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bennett R.D., Murphy B.D.;
 RT "Stem cell factor in the mink uterus";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF323757; AAK73366.1; -.
 SQ SEQUENCE 260 AA; 29542 MW; A63111CE48A50A34 CRC64;

Query Match

Best Local Similarity 73.8%; Score 725.5; DB 6; Length 260;
 Matches 144; Conservative 21; Mismatches 21; Indels 9; Gaps 2;

QY 1 MKKTQWITLCIYQLLLFNPLVTEGICRNRVTNNVNDVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITLCIYQLLLFNPLVTEGICRNRVTNNVNDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISVMYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCWISVMYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSKSPPEPRLFTPEEPFRIRNRSIDAFKDF-VVASSETSDCVSSTISPEKDSVST 179
 DB 121 ENVKSKSPKPEPRLFTPEEPFRIRNRSIDAFKDFEMVYVQSDSLTDLDFKFSNISEGLSNYSIIDKLIVDDLVECKENSS 179
 QY 180 TKPFMLPVVAASLR 194
 DB 180 -----PLGDSNLQ 187

RESULT 15

QY 092ZET PRELIMINARY; PRT: 245 AA.
 AC 092ZET;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE STEM CELL FACTOR KL-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Teramoto T., Nagashima M., Thorgerirsson S.S.;
 RT "Rat-SCF-KL-2";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF071205; AAD02828.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 SQ SEQUENCE 245 AA; 27691 MW; 961511DAA6AE4F82 CRC64;

Query Match

Best Local Similarity 79.8%; Score 721; DB 11; Length 245;
 Matches 138; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYQLLLFNPLVTEGICRNRVTNNVNDVTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITLCIYQLLLFNPLVTEGICRNRVTNNVNDVTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISVMYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 DB 61 MDVLPSCWISVMYVQSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECKENSS 120
 QY 121 KDLKSKSPPEPRLFTPEEPFRIRNRSIDAFKDFEMVYVQSDSLTDLDFKFSNISEGLSNYSIIDKLIVDDLVECKENSS 173
 DB 121 KNVKSILKPEPRLFTPEEPFRIRNRSIDAFKDFEMVYVQSDSLTDLDFKFSNISEGLSNYSIIDKLIVDDLVECKENSS 173

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OM protein - protein search, using sw model

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(without alignments)
271.883 Million cell updates/sec

Title: US-09-604-325a-61

Perfect score: 1397
Sequence: 1 MKKTQWILFCIYLQLLFN.....NEEDNEISMLQEKREKREGEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_032802.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
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19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397	100.0	273	12	AA11711
2	1397	100.0	273	13	AA11711
3	1397	100.0	273	13	AA11711
4	1397	100.0	273	18	AA11711
5	1397	100.0	273	21	AA11711
6	1397	100.0	273	22	AA11711
7	1397	100.0	273	22	AA11711
8	1397	100.0	273	22	AA11711
9	1397	100.0	273	22	AA11711
10	1397	100.0	273	22	AA11711
11	1397	100.0	273	22	AA11711

ALIGNMENTS

RESULT	1	AA11711	standard; Protein; 273 AA.
ID	AA11711	standard; Protein; 273 AA.	
AC	AA11711		
XX			
DT	20-JUN-1991	(first entry)	
DE	Human Stem Cell Factor from HT1080 fibrosarcoma line.		
XX			
KW	Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..25	
FT	Protein	/label= sig-peptide	
FT		26..273	
XX		/label= mat-protein	
XX			
XX	EP423980-A.		
XX			
XX	24-APR-1991.		
XX			
XX	04-OCT-1990.	90EP-0310899.	
XX			
XX	01-OCT-1990.	90US-0589701.	
XX	16-OCT-1989.	89US-0422383.	
XX	11-JUN-1990.	90US-0537198.	
XX	24-AUG-1990.	90US-0573616.	
XX	28-SEP-1990.	90WC-US05548.	
XX			
XX	(AMGE-) AMGEN INC.		

12	1397	100.0	273	22	AA11711	Human stem cell fa
13	1397	100.0	273	22	AA11711	Human stem cell fa
14	1397	100.0	273	22	AA11711	Human stem cell fa
15	1397	99.6	273	22	AA11711	Human stem cell fa
16	1397	99.6	273	22	AA11711	Human stem cell fa
17	1397	99.6	273	22	AA11711	Human stem cell fa
18	1397	99.6	273	22	AA11711	Human stem cell fa
19	1397	99.6	273	22	AA11711	Human stem cell fa
20	1388	99.6	273	22	AA11711	Human stem cell fa
21	1381	98.9	273	22	AA11711	Human stem cell fa
22	1381	98.9	273	22	AA11711	Human stem cell fa
23	1381	98.9	273	22	AA11711	Human stem cell fa
24	1381	98.9	273	22	AA11711	Human stem cell fa
25	1381	98.9	273	22	AA11711	Human stem cell fa
26	1378	98.6	273	22	AA11711	Human stem cell fa
27	1378	98.6	273	22	AA11711	Human stem cell fa
28	1378	98.6	273	22	AA11711	Human stem cell fa
29	1378	98.6	273	22	AA11711	Human stem cell fa
30	1378	98.6	273	22	AA11711	Human stem cell fa
31	1378	98.6	273	22	AA11711	Human stem cell fa
32	1378	98.6	273	22	AA11711	Human stem cell fa
33	1378	98.6	273	22	AA11711	Human stem cell fa
34	1378	98.6	273	22	AA11711	Human stem cell fa
35	1378	98.6	273	22	AA11711	Human stem cell fa
36	1378	98.6	273	22	AA11711	Human stem cell fa
37	1378	98.6	273	22	AA11711	Human stem cell fa
38	1378	98.6	273	22	AA11711	Human stem cell fa
39	1378	98.6	273	22	AA11711	Human stem cell fa
40	1378	98.6	273	22	AA11711	Human stem cell fa
41	1378	98.6	273	22	AA11711	Human stem cell fa
42	1378	98.6	273	22	AA11711	Human stem cell fa
43	1378	98.6	273	22	AA11711	Human stem cell fa
44	1378	98.6	273	22	AA11711	Human stem cell fa
45	1378	98.6	273	22	AA11711	Human stem cell fa

PI Zeebo KM, Suggs SV, BosseIman RA, Martin FH;
 XX
 DR WPI; 1991-119233/17.
 DR N-PSDB; AAQ11542.
 XX
 XX New naturally-occurring polypeptide stem cell factor analogues -
 PT have haematopoietic biological activity of stem cell factor and
 PT are used to treat eg leukopenia, AIDS, nerve damage and
 PT infertility
 PS Disclosure; Fig 42; 127pp; English.
 XX
 XX The SCF has the ability to stimulate growth of primitive
 CC progenitors including early hematopoietic progenitor cells and non-
 CC hematopoietic stem cells such as neural stem cells and primordial
 CC germ stem cells. The product may be used in a pharmaceutical
 CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,
 CC anaemia, AIDS, neoplasia, nerve damage, infertility and
 CC intestinal damage.
 CC See also AAR11708, AAQ11509-011543.
 CC
 XX
 SO Sequence 273 AA;
 Query Match 100.0%; Score 1397; DB 12; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCITLYQLLFPNPLVTEGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 DB 1 mktqtwilctilyqllfnpvktegicrnrvtnvkvdklvanylpxdymitlkyypg 60
 QY 61 MDVLPSCHEWVWVQVSDSLTDLDFKSNISSEGLSNYSIIDKLVNIYDDIVECKENSS 120
 DB 61 mdvlpshcwsemvvgdsldldkfnsiseglsnysiidklniyddiveckens 120
 QY 121 KDUKSFKSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 DB 121 kdksfksperrlftpeeffrinfnsidafkdfvvasetsdcvvsstlspkdsrvsvt 180
 QY 121 kdksfksperrlftpeeffrinfnsidafkdfvvasetsdcvvsstlspkdsrvsvt 180
 QY 181 KPFLMPVPAASLRDSSSNRKAKNPGRGSSLHMAAMALPALFSLITGFAGALYWKRR 240
 DB 181 kpflmpvpaaslrndsssnrkaknpgrgsslhmaamalpalfsliigfagalwykr 240
 QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
 DB 241 qpsltraveniqineedneismloekerefoev 273
 RESULT 2
 AAR20647
 ID AAR20647 standard; Protein; 273 AA.
 XX
 AC AAR20647;
 XX
 DT 30-APR-1992 (first entry)
 XX
 DE Human mast cell growth factor.
 XX
 KW hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene;
 KW proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= signal
 FT Region 26..210
 FT /label= extracellular
 FT /note= "claimed polypeptide"
 FT Region 211..237
 FT /label= transmembrane
 FT Region 238..273

FT
 XX
 PN W09200376-A.
 XX
 PD 09-JAN-1992.
 XX
 PF 14-JUN-1991; 91WO-US04274.
 XX
 PR 25-JUN-1990; 90US-0543264.
 PR 10-AUG-1990; 90US-0565840.
 PR 28-AUG-1990; 90US-0574152.
 PR 21-SEP-1990; 90US-0586073.
 PR 12-JUN-1991; 91US-0713715.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Williams DE, Lyman S;
 XX
 DR WPI; 1992-041558/05.
 DR N-PSDB; AAQ20845.
 XX
 XX New isolated DNA encoding human mast cell growth factor - useful in
 PT stimulating proliferation of haematopoietic cells with growth factor,
 PT to treat haemolytic and hypoproliferative anaemias
 PS Claim 10; Fig 4; 59pp; English.
 XX
 XX This human MGF has a mature extracellular region of 185 amino acids.
 CC There is a second form of hMGF (see AAQ20844) resulting from an
 CC alternative mRNA splicing event which deletes an exon encoding an
 CC additional 28 amino acids beginning at amino acid 148 of the mature
 CC protein. MGF is the ligand for the protein receptor expression product
 CC of the c-kit proto-oncogene. MGF can be used to augment the
 CC activity of other cytokines. It can influence early lymphoid or
 CC myeloid development. See also AAQ20842-3 and AAQ22204-7.
 CC
 XX
 SO Sequence 273 AA;
 Query Match 100.0%; Score 1397; DB 13; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKTQWILTCITLYQLLFPNPLVTEGICRNRVTNNVKDVKLVANLPKDYMITLKYPG 60
 DB 1 mktqtwilctilyqllfnpvktegicrnrvtnvkvdklvanylpxdymitlkyypg 60
 QY 61 MDVLPSCHEWVWVQVSDSLTDLDFKSNISSEGLSNYSIIDKLVNIYDDIVECKENSS 120
 DB 61 mdvlpshcwsemvvgdsldldkfnsiseglsnysiidklniyddiveckens 120
 QY 121 KDUKSFKSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPKDSRVSVT 180
 DB 121 kdksfksperrlftpeeffrinfnsidafkdfvvasetsdcvvsstlspkdsrvsvt 180
 QY 121 kdksfksperrlftpeeffrinfnsidafkdfvvasetsdcvvsstlspkdsrvsvt 180
 QY 181 KPFLMPVPAASLRDSSSNRKAKNPGRGSSLHMAAMALPALFSLITGFAGALYWKRR 240
 DB 181 kpflmpvpaaslrndsssnrkaknpgrgsslhmaamalpalfsliigfagalwykr 240
 QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
 DB 241 qpsltraveniqineedneismloekerefoev 273
 RESULT 3
 AAR83978
 ID AAR83978 standard; Protein; 273 AA.
 XX
 AC AAR83978;
 XX
 DT 15-MAY-1996 (first entry)
 XX
 DE Human stem cell factor derived from HT1080 fibrosarcoma cell line.

XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
 KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= sig-peptide
 FT 26..248
 FT Protein /label= mat-SCF
 XX EP67470-A1.
 XX 11-OCT-1995.
 XX 04-OCT-1990; 90EP-0105391.
 XX 01-OCT-1990; 90US-0589701.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90WO-0505548.
 XX (AMGE-) AMGEN INC.
 XX Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
 DR WPI: 1995-346090/45.
 DR N-PSDB; AAT04890.
 XX New stem cell factor polypeptide(s) - for stimulating the growth of
 PT primitive progenitor cells, esp. for treating disorders involving
 PT blood cells
 XX Claim 9; Fig 42; 127bp; English.
 XX AAR83978 is a human stem cell factor (SCF) derived from the HT1080
 CC fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as haematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leucopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 XX Sequence 273 AA:
 SQ

Query Match 100.0%; Score 1397; DB 16; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRTQWILTCIYQLLEFNPLVTEGICRNVRVNNVKDVTKLVANLPKDYMITLKYPG 60
 DB 1 mktqtwtlctiyqllefnplvtegicrnvrnnvkdvtklvannlpkdymitlkyppg 60
 QY 61 MDVLSHCWISDMVYVQSDSLFDLDKFSNISSEGLSNTSIIDKLNIYVDLVECKENSS 120
 DB 61 mdvlschcwisdmvyvqsdslfdldkfsnisseglsnysiidklniyvddlveckenss 120
 QY 121 KDLKSFKSPERLFTPEEFRIFNRSIDAFKDFVASTSCVYSSNTLSPKDSRVSVT 180
 DB 121 kdlksfksperlftpeefrifnrsidafkdfvastscvysntlspekdsrsvt 180
 DB 121 kdlksfksperlftpeefrifnrsidafkdfvastscvysntlspekdsrsvt 180

QY 181 KPFMLPVAASSLINDSSSNRKAKNPBGSSLSHMAAMALPAIFSLITGFAGALYKKR 240
 DB 181 kpfmlpvaasslindsssnrkkaknpbgssslshmaamalpalifslitgfagalykkrr 240
 QY 241 QPSLTRAVENTIQINDEEDNEISMLQEKEREFOEV 273
 DB 241 qpsltraveniqinneedneismlqekerefev 273
 RESULT 4
 ID AAM27607 standard; Protein; 273 AA.
 XX AAM27607;
 AC AAM27607;
 DT 28-APR-1998 (first entry)
 DE Human recombinant stem cell factor protein.
 KW Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
 KW SF; Sulf; analogue; treatment; haematopoietic factor; progenitor cell;
 KW pigmentation disorder; haematopoietic disorder.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= leader sequence
 FT 26..274
 FT Protein /note= "mature full length stem cell factor protein"
 XX W09738101-A1.
 XX 16-OCT-1997.
 XX 03-APR-1997; 97WO-US05541.
 XX 05-APR-1996; 96US-0628428.
 XX (AMGE-) AMGEN INC.
 XX Lu HS;
 DR WPI: 1997-512718/47.
 XX Stem cell factor analogue NI0D or NI0D/NI1D - useful to treat
 PT pigmentation disorder, AIDS, nerve damage, infertility, intestinal
 PT damage or haematopoietic disorder
 XX Claim 2; Fig 1; 42pp; English.
 XX This sequence represents a membrane bound form of a human recombinant
 CC stem cell factor (SCF). Stem cell factors are also known as mast cell
 CC growth factors (MCGF) or Steel factors (SF or Sulf) are haematopoietic
 CC factors which act on haematopoietic progenitor cells. Analogues of a
 CC wild type SCF sequence have been constructed (see AAM27605 and AAM27606)
 CC which have increased biological activity and stability compared to
 CC unmodified SCF and can be used to treat pigmentation disorders, e.g.
 CC vitiligo, acquired immunodeficiency syndrome, nerve damage, infertility,
 CC intestinal damage or a haematopoietic disorder, e.g. leucopenia,
 CC thrombocytopenia or anaemia, enhance bone marrow engraftment during
 CC transplantation or bone marrow recovery following radiation, chemical or
 CC chemotherapeutic, induced bone marrow aplasia or myelosuppression,
 CC sensitive cells to chemotherapy or mobilise peripheral blood progenitor
 CC cells. It can also be used in an in vitro haematopoietic cell, preferably
 CC bone marrow or peripheral blood progenitor cell, culture medium, where
 CC the cells are optionally subsequently transfected with exogenous DNA.
 XX Sequence 273 AA:
 SQ

Query Match 100.0%; Score 1397; DB 16; Length 273;

Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYTNVKKVYKLVANLPDYMITLKYPG 60
Db 1 mktqwtlctiyqllfnpvlklegicrnrvtnvkvkvlvankpdkymtlkypg 60
QY 61 MDVLPSCWISSEWVQVSDSLDLDKFSNISEGLSNYSIIIRKLVNIYVDLVCVENSS 120
Db 61 mdvlpschwissewvqvsdsltldkfsniseglsnysliidrklniyvdlvcvenss 120
QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDVVASSETSDCVSSTLSPKDSRVSYT 180
Db 121 kdlksfksperplftpeeffrifnrsidafkdvvasetsdcvssstlspkdsrvsytl 180
QY 181 KPEMLPPVAASLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLITGFAGALYWKRR 240
Db 181 kpemlppvaaslrndsssnrkaknpqdsllhwaamalpalfslltfgalylwkkrr 240
QY 241 QPSLTRAVENTQINEDNEISMLOEKERFQEV 273
Db 241 qpsltraveniqinedneismloekerefgev 273

RESULT 5
AAV53284
ID AAV53284 standard; Protein; 273 AA.
XX
AC AAV53284;
XX
DT 27-JUL-2000 (first entry)
XX
XX Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
XX
XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW primitive progenitor cell; haematopoietic disorder; synergistic;
KW allogenic; autologous bone marrow transplant; gene therapy;
KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
cancer.
XX
OS Homo sapiens.
XX
PN EP992579-A1.
XX
PD 12-APR-2000.
XX
PF 04-OCT-1990; 99EP-0122861.
XX
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90MO-US05548.
PR 01-OCT-1990; 90US-0589701.
PR 04-OCT-1990; 90EP-0310899.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosseimann RA, Martin FH;
XX
DR WPI: 2000-259135/23.
DR N-PSDB; AAA13714.
XX
PT Production of hematopoietic cells suitable for administration to a
PT subject using progenitor cells and expanding the cells using stem cell
PT factor -
XX
PS Claim 22; Fig 42; 123pp; English.
XX
XX A method has been developed of making haematopoietic cells suitable for
CC administration to a subject. The method comprises: (a) obtaining
CC haematopoietic progenitor cells from a donor; and (b) expanding the
CC cells by adding to the cells a haematopoietically effective dose of a
CC polypeptide product having at least part of the primary structural

CC confirmation and one or more of the biological properties of naturally
CC occurring stem cell factor (SCF). The method is useful for stimulating
CC primitive progenitor cells including early hematopoietic progenitor
CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is
CC useful for expanding early haematopoietic progenitors in syngeneic,
CC allogeneic or autologous bone marrow transplant. SCF is useful for
CC enhancing the efficiency of gene therapy based on transfecting the
CC haematopoietic stem cells. SCF is also useful for combating the
CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
CC haematopoietic recovery after acute blood loss and as a boost to the
CC immune system for fighting neoplasia (cancer). The present sequence
CC represents a specifically claimed human SCF from the present invention.
XX
SO Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPLVKTGICRNRYTNVKKVYKLVANLPDYMITLKYPG 60
Db 1 mktqwtlctiyqllfnpvlklegicrnrvtnvkvkvlvankpdkymtlkypg 60
QY 61 MDVLPSCWISSEWVQVSDSLDLDKFSNISEGLSNYSIIIRKLVNIYVDLVCVENSS 120
Db 61 mdvlpschwissewvqvsdsltldkfsniseglsnysliidrklniyvdlvcvenss 120
QY 121 KDLKSFSPERPLFTPEEFRIFNRSIDAFKDVVASSETSDCVSSTLSPKDSRVSYT 180
Db 121 kdlksfksperplftpeeffrifnrsidafkdvvasetsdcvssstlspkdsrvsytl 180
QY 181 KPEMLPPVAASLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLITGFAGALYWKRR 240
Db 181 kpemlppvaaslrndsssnrkaknpqdsllhwaamalpalfslltfgalylwkkrr 240
QY 241 QPSLTRAVENTQINEDNEISMLOEKERFQEV 273
Db 241 qpsltraveniqinedneismloekerefgev 273

RESULT 6
AAU05266
ID AAU05266 standard; Protein; 273 AA.
XX
AC AAU05266;
XX
DT 24-OCT-2001 (first entry)
XX
XX Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
XX
XX Human; stem cell factor; SCF; haematopoietic progenitor cell; AIDS;
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW hypopigmentation disorder; viral disorder; HT1080 fibrosarcoma.
XX
OS Homo sapiens.
XX
FH Key
FT Protein
FT 1..25 Location/Qualifiers
FT /label= signal_peptide
FT 26..273
FT /label= Mature_SCF
FT Misc-difference 97
FT /note= "Encoded by ATT"
FT Misc-difference 258
FT /note= "Encoded by ATT"
XX
PN US6248319-B1.
XX
PD 19-JUN-2001.


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XX 24-MAY-1995; 95US-0449653.
XX
PR 10-APR-1991; 91US-0684535.
PR 25-NOV-1992; 92US-0962255.
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 01-OCT-1990; 90US-0589701.
PR 21-DEC-1993; 93US-012329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOS/) BOSSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI: 2001-407312/43.
DR N-PSDB: AAS10461.
XX
PT Increasing the number of early haematopoietic progenitor cells in the
PT peripheral blood useful for the treatment of blood disorders including
PT Hodgkin's disease comprises the administration of human stem cell
PT factor -
XX
XX Example 3; Fig 42; 210pp; English.
XX
CC The present sequence represents human stem cell factor (SCF). The cDNA
CC encoding this sequence is isolated from the HT1080 fibrosarcoma cell
CC line. The sequence is described in an invention relating to novel stem
CC cell factors, the polynucleotides encoding them and methods for
CC producing the stem cell factors. The methods involve increasing the
CC number of early haematopoietic progenitor cells in human peripheral
CC blood by administering a haematopoietically effective human stem cell
CC factor polypeptide. The methods are useful for the treatment of blood
CC disorders, including myelofibrosis, myelocystosis, osteopetrosis,
CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
CC anaemia, malaria, vitamin B12 and folic acid deficiency,
CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
CC including AIDS.
CC
XX
SQ Sequence 273 AA:

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```

Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MKKTQWILTCIYLOLLFNPLVKTGICRNRYNNKVDYKLVANLPKDYMITLKYVG 60
DB 1 mktqtwtlctiyqlilfnplvktgicrnrynnkvdylvanlpkdymitlkyvg 60
QY 61 MDVLPSCWISSEMYVOLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 mdvlpshcwisemvolsdsltldldkfsniseglsnysiidklyniyvdllvecvkens 120
QY 121 KDLKSFKSPERLFTPEEFRIKRSIDAFKDFVVASSETSDCVVSTLSPKDSRVSVT 180
DB 121 kdlksfksperrlftpeeffrikrsidafkdfvvasetsdcvvsstlspkdsrvsvt 180
QY 181 KPFMLPVAASSLRNDSSSNKRAKNPGDSSLHMAAMALPALFSLITIGFAGALYWKRR 240
DB 181 kpfmlpvaasslrndsssnkrapgdsllhwaamalpaltsliligtalgalwykrr 240
QY 241 QPSLTRAVENTIOINEDNEISMLOKEREFOEV 273
DB 241 qpsltraveniqineedneismloqekerefev 273

```

RESULT 7
AAB98357

```

ID AAB98357 standard; Protein; 273 AA.
XX
AC AAB98357;
XX
DT 21-AUG-2001 (first entry)
XX
DE Human SCF protein SEQ ID NO:49.
XX
KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US6207454-B1.
XX
PD 27-MAR-2001.
XX
PF 31-DEC-1998; 98US-0224681.
XX
PR 21-DEC-1993; 93US-0172329.
PR 24-MAY-1995; 95US-0449653.
PR 12-JAN-1998; 98US-0005893.
PR 25-NOV-1992; 92US-0982255.
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 01-OCT-1990; 90US-0589701.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI: 2001-36062/38.
XX
PT Enhancing efficiency of transfer of polynucleotide into a target
PT mammalian cell in vitro, involves exposing cell that expresses a stem
PT cell factor receptor to stem cell factor, and introducing
PT polynucleotide into cell in vitro -
XX
XX Example 3; Fig 16; 210pp; English.
XX
CC The present invention describes a method for enhancing (E) the
CC efficiency of transfer of a polynucleotide (I) into a target mammalian
CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
CC factor (SCF) receptor to a biologically active SCF, its analogue or
CC fragment, which induces cell proliferation, and introducing (I) to (II)
CC into the cell. The method is useful for enhancing the efficiency of the
CC transfer of a polynucleotide into a target mammalian cell in vitro.
CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
CC and AAB98351 to AAB98390 represent sequences used in the exemplification
CC of the present invention.
CC
XX
SQ Sequence 273 AA:

```

```

Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MKKTQWILTCIYLOLLFNPLVKTGICRNRYNNKVDYKLVANLPKDYMITLKYVG 60
DB 1 mktqtwtlctiyqlilfnplvktgicrnrynnkvdylvanlpkdymitlkyvg 60
QY 61 MDVLPSCWISSEMYVOLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIYVDLVECVKENS 120
DB 61 mdvlpshcwisemvolsdsltldldkfsniseglsnysiidklyniyvdllvecvkens 120
QY 121 KDLKSFKSPERLFTPEEFRIKRSIDAFKDFVVASSETSDCVVSTLSPKDSRVSVT 180
DB 121 kdlksfksperrlftpeeffrikrsidafkdfvvasetsdcvvsstlspkdsrvsvt 180
QY 181 KPFMLPVAASSLRNDSSSNKRAKNPGDSSLHMAAMALPALFSLITIGFAGALYWKRR 240
DB 181 kpfmlpvaasslrndsssnkrapgdsllhwaamalpaltsliligtalgalwykrr 240

```

```

Db      181 kpfmlppvaasslrndsssnrkaknpgdsslhwaamalpalflsligfagalywkkrr 240
QY      241 QPSLTRAVENIQINEEDNEISMLOEKEREQEV 273
Db      241 qpsltraveniqineedneismloekereqev 273

RESULT 8
AAB98367
ID      AAB98367 standard; Protein: 273 AA.
XX
AC      AAB98367;
XX
DE      21-AUG-2001 (first entry)
XX
DE      Human SCF protein sequence SFQ ID NO:61.
XX
KW      Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW      gene therapy.
XX
OS      Homo sapiens.
XX
PN      US6207454-B1.
XX
PD      27-MAR-2001.
XX
PE      31-DEC-1998; 98US-0224681.
XX
PR      21-DEC-1993; 93US-0172329.
PR      24-MAY-1995; 95US-0449653.
PR      12-JAN-1998; 98US-0005893.
PR      25-NOV-1992; 92US-0982255.
PR      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      01-OCT-1990; 90US-0589701.
XX
PA      (AMGE-) AMGEN INC.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX      WPI: 2001-366062/38.
XX      N-PSDB; AAH41344.
XX
PT      Enhancing efficiency of transfer of polynucleotide into a target
PT      mammalian cell in vitro, involves exposing cell that expresses a stem
PT      cell factor receptor to stem cell factor, and introducing
PT      polynucleotide into cell in vitro -
XX
PS      Claim 17; Fig 42; 210pp; English.
XX
XX      The present invention describes a method for enhancing (E) the
XX      efficiency of transfer of a polynucleotide (I) into a target mammalian
XX      cell (II) in vitro, comprising exposing (II) that expresses a stem cell
XX      factor (SCF) receptor to a biologically active SCF, its analogue or
XX      fragment, which induces cell proliferation, and introducing (I) to (II)
XX      in vitro. Exposure of SCF to (II) results in increased uptake of (I)
XX      into the cell. The method is useful for enhancing the efficiency of the
XX      transfer of a polynucleotide into a target mammalian cell in vitro.
XX      The method is useful in gene therapy techniques. AAH41301 to AAH41364
XX      and AAB98351 to AAB98390 represent sequences used in the exemplification
XX      of the present invention.
XX
SQ      Sequence 273 AA:

```

```

Query Match      100.0%; Score 1397; DB 22; Length 273;
Best local Similarity 100.0%; Pred. No. 2,8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MKKTGWTLCITLQLLRPVLTGTCGRNRTNNVAVTKLVANLPRDWTITLKYPVG 60

```

```

Db      1 mktqwtlltctylqllfnplvkktegiocrnrvnnykdvcklvianlpkdymltkyvpq 60
QY      61 MDVPSHCWISBMYVQLSDSLTDLIDKFSNISEGLSNVSTIDKLYNVVDLVECVKENS 120
Db      61 mdvlpshcwisemvqslsdsltdlidsniseqlsnvstldklynvvdldvecvkens 120
QY      121 KDIKSFSPSPRLPTPEEPFRIFNRSIDAFKDVVASETSDCVVSSSTLSPKDSRVSVT 180
Db      121 KDIKSFSPSPRLPTPEEPFRIFNRSIDAFKDVVASETSDCVVSSSTLSPKDSRVSVT 180
QY      181 KPFLMPVVAASSLRNDSSSNRKAKNPPGSSLHWAMALPALSLIIGFAGLYWKKRR 240
Db      181 kpfmlppvaasslrndsssnrkaknpgdsslhwaamalpalflsligfagalywkkrr 240
QY      241 QPSLTRAVENIQINEEDNEISMLOEKEREQEV 273
Db      241 qpsltraveniqineedneismloekereqev 273

```

```

RESULT 9
AA002460
ID      AA002460 standard; Protein: 273 AA.
XX
AC      AA002460;
XX
DE      29-AUG-2001 (first entry)
XX
DE      Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
XX
KW      Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW      anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
KW      HT1080 fibrosarcoma.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      Protein 1..25
FT      Protein /label= Signal_peptide
FT      Protein 26..273
FT      Protein /label= Mature_SCF
XX
PN      US6207417-B1.
XX
PD      27-MAR-2001.
XX
PE      07-JUN-1995; 95US-0482918.
XX
PR      21-DEC-1993; 93US-0172329.
PR      16-OCT-1989; 89US-0422383.
PR      11-JUN-1990; 90US-0537198.
PR      24-AUG-1990; 90US-0573616.
PR      01-OCT-1990; 90US-0589701.
XX
PA      (ZSEBO/) ZSEBO K M.
PA      (BOSS/) BOSSELMAN R A.
PA      (SUGG/) SUGGS S V.
PA      (MART/) MARTIN F H.
XX
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX      WPI: 2001-298941/31.
XX      N-PSDB; AAS04124.
XX
XX      Novel nucleic acids encoding stem cell factor useful for treating
XX      disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
XX      disease, kala azar, anaemia and septicemia -
XX
XX      Example 5; Fig 42A-42C; 209pp; English.
XX
XX      The present sequence representing human SCF (stem cell factor) protein
XX      is isolated from the HT1080 fibrosarcoma cell line. The present invention
XX      relates to novel stem cell factors (AA002453-AA002458, AA002461) and

```

CC the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.
 CC
 XX Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPKVTEGICRNRVTNNKVDYTKLVANPKRYMTTKYVP 60
 Db 1 mktqtwilctciyqlllfnplvktegicrnrvtnnvkdvtklvannpkdytmilkyvp 60
 QY 61 MDVLPSCWISEMNVQSLDLSLTLDFKFSNISEGINSYTIIDKLVNIYDVLVECKENS 120
 Db 61 mdvlpshcwisemvqslsdltldkfnsniseglnsytlidklvniydvdlveckens 120
 QY 121 KDLSKFSKSPPEPLTPPEEFRRIFNRSIDAFKDFVAVASETSDCVSSSTLSPEKDSRVSVT 180
 Db 121 kdlskfskspeprltppeefrrifnrsidafkdfvavasetscvssstlspekdsrvsvt 180
 QY 181 KPFLMPVPAASSLRNDSSSNRRKAKNPGGSSLHMAAMALPALFSLITIGAFGALYWKRR 240
 Db 181 kpflmpvpaasslrndsssnrrkaknpggsslhmaamalpalfslitigafgalywkr 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273
 Db 241 qpsltraveniqineedneismleqerfgev 273

RESULT 10
 AAU02766
 ID AAU02766 standard; Protein; 273 AA.

AC AAU02766;
 DT 29-AUG-2001 (first entry)

DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW HT1080 fibrosarcoma.
 XX

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Protein 1..25
 FT /label= Signal_peptide
 FT Protein 26..273
 FT /label= Mature_SCF

XX US6218148-B1.
 XX 17-APR-2001.
 XX 21-DEC-1993; 93US-0172329.
 XX 25-NOV-1992; 92US-0982255.
 XX 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 PA (AMGE-) AMGEN INC.

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-281051/29.
 DR N-PSDB; AAS04224.
 XX

PT Isolated DNA sequence, encoding polypeptide product useful for
 PT stimulating growth of early haematopoietic progenitor cells -
 XX
 PS Example 5; Fig 42A-42C; 167pp; English.

XX The present sequence representing human SCF (stem cell factor) protein
 CC is isolated from the HT1080 fibrosarcoma cell line. The present
 CC invention relates to novel stem cell factors
 CC (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
 CC encoding them. SCF stimulate primitive progenitor cells including early
 CC haematopoietic progenitor cells. The invention also describes SCF
 CC peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04218) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing
 CC SCF and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.
 CC
 XX Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLFPNPKVTEGICRNRVTNNKVDYTKLVANPKRYMTTKYVP 60
 Db 1 mktqtwilctciyqlllfnplvktegicrnrvtnnvkdvtklvannpkdytmilkyvp 60
 QY 61 MDVLPSCWISEMNVQSLDLSLTLDFKFSNISEGINSYTIIDKLVNIYDVLVECKENS 120
 Db 61 mdvlpshcwisemvqslsdltldkfnsniseglnsytlidklvniydvdlveckens 120
 QY 121 KDLSKFSKSPPEPLTPPEEFRRIFNRSIDAFKDFVAVASETSDCVSSSTLSPEKDSRVSVT 180
 Db 121 kdlskfskspeprltppeefrrifnrsidafkdfvavasetscvssstlspekdsrvsvt 180
 QY 181 KPFLMPVPAASSLRNDSSSNRRKAKNPGGSSLHMAAMALPALFSLITIGAFGALYWKRR 240
 Db 181 kpflmpvpaasslrndsssnrrkaknpggsslhmaamalpalfslitigafgalywkr 240
 QY 241 QPSLTRAVENIQINEEDNEISMLQEKERFQEV 273
 Db 241 qpsltraveniqineedneismleqerfgev 273

RESULT 11
 AAB73567
 ID AAB73567 standard; Protein; 273 AA.

AC AAB73567;
 DT 07-AUG-2001 (first entry)

DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.
 KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 XX

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPVTEGICRNRTNNKVDYTKLVANLPKDYMITLKYPG 60
 DB 1 mkkqtwtlctciyqlllfnplvtegcicrnrvtnnvkdvtklvannlpkdymitlkypg 60

QY 61 MDVLPSCWISSEMYVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVIYDDIVECVKENS 120
 DB 61 mdvlpshcwissemvqgsdsltldkfniseglsnysliidklvlnvddivecvkens 120

QY 121 KDLKSKSPSPRLTPPEEFRIFRNSIDA FKDFVVASETSDCVSSSTLSPKDSRVS 180
 DB 121 kdlkksfkspeprltfpeefrfrnsida fkd fva setsdcvssstlspekdsrvsvt 180

QY 181 KPFMLPVAASSLRNDSSSNRKA KNP GDS SLHMAA MALPALFSLIIGFAGALYWK 240
 DB 181 kpfmlpvaasslrndsssnrkaknp gds slhmaa malpalfslligfagalwykkr 240

QY 241 QPSLTRA VENIQINEEDNEISMLOEKEREFOEV 273
 DB 241 qpsltraveniqineedneismlogekerefgev 273

RESULT 13
 AAB96942
 ID AAB96942 standard; Protein; 273 AA.
 XX AAB96942;
 AC AAB96942;
 XX
 DT 13-JUL-2001 (first entry)
 DE Human stem cell factor SEQ ID NO: 49.
 XX
 KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;
 KW severe combined immunodeficiency.
 XX
 OS Homo sapiens.
 XX
 PN US6207802-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 09-NOV-1994; 94US-0336728.
 XX
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-353108/37.
 XX
 PT Novel isolated non-human mammalian stem cell factor polypeptide
 PT stimulating growth of early haematopoietic progenitor cells; useful for
 PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
 PT sarcoidosis -
 XX
 PS Example 3; Fig 16; 209pp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the
 CC growth of early haematopoietic progenitor cells, neural stem cells and
 CC primordial germ stem cells. The sequences are useful in the treatment of
 CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological

CC and intestinal damage, infertility, AIDS and severe combined
 CC immunodeficiency (SCID). The present sequence is an SCF described in the
 CC invention.
 CC
 XX
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1397; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.8e-133;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPVTEGICRNRTNNKVDYTKLVANLPKDYMITLKYPG 60
 DB 1 mkkqtwtlctciyqlllfnplvtegcicrnrvtnnvkdvtklvannlpkdymitlkypg 60

QY 61 MDVLPSCWISSEMYVQSDSLTDLLDKFSNISSEGLSNYSIIDKLVIYDDIVECVKENS 120
 DB 61 mdvlpshcwissemvqgsdsltldkfniseglsnysliidklvlnvddivecvkens 120

QY 121 KDLKSKSPSPRLTPPEEFRIFRNSIDA FKDFVVASETSDCVSSSTLSPKDSRVS 180
 DB 121 kdlkksfkspeprltfpeefrfrnsida fkd fva setsdcvssstlspekdsrvsvt 180

QY 181 KPFMLPVAASSLRNDSSSNRKA KNP GDS SLHMAA MALPALFSLIIGFAGALYWK 240
 DB 181 kpfmlpvaasslrndsssnrkaknp gds slhmaa malpalfslligfagalwykkr 240

QY 241 QPSLTRA VENIQINEEDNEISMLOEKEREFOEV 273
 DB 241 qpsltraveniqineedneismlogekerefgev 273

RESULT 14
 AAB96952
 ID AAB96952 standard; Protein; 273 AA.
 XX AAB96952;
 AC AAB96952;
 XX
 DT 13-JUL-2001 (first entry)
 DE Human stem cell factor SEQ ID NO: 61.
 XX
 KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;
 KW severe combined immunodeficiency.
 XX
 OS Homo sapiens.
 XX
 PN US6207802-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 09-NOV-1994; 94US-0336728.
 XX
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-353108/37.
 XX
 DR N-PSDB; AAF89104.

```

XX
PT Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early haematopoietic progenitor cells, useful for
PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis -
XX
PS Example 3; Fig 42; 209pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early haematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is an SCF described in the
CC invention.
CC
XX
SQ Sequence 273 AA;
XX
Query Match 100.0%; Score 1397; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKKQTWTLTCIYQLLFPNPKVTEGICRNRYTNVWKDVTKLVANLPKDYMITLKYPG 60
DB 1 mkkqtwtlctiyqlilfnpvklegicrntvnmkvdklvaniipkdymitlkypg 60
QY 61 MDVLPSCWISSENVVOLSLSLTLDLKFSNISSEGLSNYSIDKLVINIVDDLVECKENSS 120
DB 61 mdvlpshcwisemvqlsdltdldkfsniseglsnysidklvinivddlveckenss 120
QY 121 KDLKSKFSPPRLFTPEEPFRIFNRSIDAKFDVVASETSDCVVSSSTLSPKDSRVSVT 180
DB 121 kdlkskfspprlftpeefrfrifnrsidakfdvvaesetdsvsstlspekdsrvsvt 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPBGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
DB 181 kpflmpvaasslrndsssnrkaknpbgdsslhmaamalpalfsliigfagalwykkr 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 qpsltraveniqineedneismlogekerefev 273
XX
RESULT 15
AAU05256
ID AAU05256 standard; Protein; 273 AA.
XX
AC AAU05256;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human stem cell factor (SCF) protein encoded by SCF gene.
XX
KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW hypopigmentation disorder; viral disorder; AIDS.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FH Peptide 1..25
FH Protein /label= Signal_peptide
FH 26..273
FH /label= Mature_SCF
XX
US6248319-B1.
XX
19-JUN-2001.
XX
24-MAY-1995; 95US-0449653.

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XX
PR 10-APR-1991; 91US-0684535.
PR 25-NOV-1992; 92US-0988255.
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 01-OCT-1990; 90US-0589701.
PR 21-DEC-1993; 93US-0172329.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGS/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI: 2001-407312/43.
DR N-PSDB: AAS10458.
XX
PT Increasing the number of early haematopoietic progenitor cells in the
PT peripheral blood useful for the treatment of blood disorders including
PT Hodgkin's disease comprises the administration of human stem cell
PT factor -
XX
PS Example 3; Fig 15D; 210pp; English.
XX
CC The present sequence represents human stem cell factor (SCF) protein
CC encoded by the SCF gene. The sequence is described in an invention
CC relating to novel stem cell factors, the polynucleotides encoding them
CC and methods for producing the stem cell factors. The methods involve
CC increasing the number of early haematopoietic progenitor cells in human
CC peripheral blood by administering a haematopoietically effective human
CC stem cell factor polypeptide. The methods are useful for the treatment
CC of blood disorders, including myelofibrosis, myelocytosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC refractory anaemia, malaria, vitamin B12 and folic acid deficiency,
CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
CC including AIDS.
CC
XX
SQ Sequence 273 AA;
XX
Query Match 99.6%; Score 1392; DB 22; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.1e-133;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MKKQTWTLTCIYQLLFPNPKVTEGICRNRYTNVWKDVTKLVANLPKDYMITLKYPG 60
DB 1 mkkqtwtlctiyqlilfnpvklegicrntvnmkvdklvaniipkdymitlkypg 60
QY 61 MDVLPSCWISSENVVOLSLSLTLDLKFSNISSEGLSNYSIDKLVINIVDDLVECKENSS 120
DB 61 mdvlpshcwisemvqlsdltdldkfsniseglsnysidklvinivddlveckenss 120
QY 121 KDLKSKFSPPRLFTPEEPFRIFNRSIDAKFDVVASETSDCVVSSSTLSPKDSRVSVT 180
DB 121 kdlkskfspprlftpeefrfrifnrsidakfdvvaesetdsvsstlspekdsrvsvt 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPBGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
DB 181 kpflmpvaasslrndsssnrkaknpbgdsslhmaamalpalfsliigfagalwykkr 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 qpsltraveniqineedneismlogekerefev 273

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Search completed: August 18, 2002, 13:08:02
 Job time: 407 sec

Sun Aug 18 14:09:03 2002

us-09-604-325a-61.rag

Page 11

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•

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:04:01 ; Search time 41.62 Seconds

(without alignments)
160.216 Million cell updates/sec

Title: US-09-604-325A-61

Perfect score: 1397
Sequence: 1 MKKTQWTLITCIYQLLFFN.....NEEDNEISMLQEKERERQEV 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents,AA:*

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	273	1	US-08-220-379B-2
2	1397	100.0	273	2	US-08-628-428-9
3	1397	100.0	273	3	US-08-482-918-49
4	1397	100.0	273	4	US-08-482-918-61
5	1397	100.0	273	4	US-09-224-681-49
6	1397	100.0	273	4	US-09-224-681-61
7	1397	100.0	273	4	US-08-336-728A-48
8	1397	100.0	273	4	US-08-336-728A-49
9	1397	100.0	273	4	US-08-336-728A-61
10	1397	99.6	273	4	US-08-482-918-48
11	1392	99.6	273	4	US-09-224-681-48
12	1381	98.9	273	4	US-08-482-918-50
13	1381	98.9	273	4	US-09-224-681-50
14	1378	98.6	273	4	US-08-336-728A-50
15	1265	90.6	248	2	US-08-955-848A-82
16	1232.5	88.2	266	4	US-08-482-918-57
17	1232.5	88.2	266	4	US-09-224-681-57
18	1232.5	88.2	266	4	US-08-336-728A-57
19	1231	88.1	245	4	US-08-482-918-63
20	1231	88.1	245	4	US-09-224-681-63
21	1231	88.1	245	4	US-08-336-728A-63
22	1202.5	86.1	274	4	US-08-482-918-51
23	1180.5	84.5	274	4	US-09-224-681-51
24	1180.5	84.5	274	4	US-08-336-728A-51
25	1179.5	84.4	271	4	US-08-482-918-52
26	1179.5	84.4	271	4	US-09-224-681-52
27	1179.5	84.4	271	4	US-08-336-728A-52

28	1178.5	84.4	274	4	US-08-336-728A-53	Sequence 53, Appl
29	1173	84.0	273	4	US-08-482-918-53	Sequence 53, Appl
30	1173	84.0	273	4	US-09-224-681-53	Sequence 53, Appl
31	1158	82.9	273	4	US-08-482-918-42	Sequence 42, Appl
32	1158	82.9	273	4	US-09-224-681-42	Sequence 42, Appl
33	1158	82.9	273	4	US-08-336-728A-42	Sequence 54, Appl
34	1158	82.9	273	4	US-08-336-728A-54	Sequence 54, Appl
35	1157	82.8	273	1	US-08-220-379B-6	Sequence 6, Appl
36	1157	82.8	273	4	US-08-482-918-55	Sequence 55, Appl
37	1157	82.8	273	4	US-09-224-681-55	Sequence 55, Appl
38	1157	82.8	273	4	US-08-336-728A-55	Sequence 55, Appl
39	1151	82.4	273	4	US-08-482-918-54	Sequence 54, Appl
40	1151	82.4	273	1	US-09-224-681-54	Sequence 54, Appl
41	1144	81.9	273	1	US-08-341-456A-11	Sequence 11, Appl
42	1144	81.9	273	3	US-08-478-414A-11	Sequence 11, Appl
43	1144	81.9	273	3	US-08-325-240A-11	Sequence 11, Appl
44	1144	81.9	273	4	US-08-898-982-11	Sequence 11, Appl
45	1030	73.7	208	4	US-08-836-252A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-220-379B-2
Sequence 2, Application US/08220379B
Patent No. 5525708
GENERAL INFORMATION:
APPLICANT: No. 5525708ka, Karl
APPLICANT: Lobell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: cleavage site
LOCATION: 164..165
US-08-220-379B-2

Query Match 100.0%; Score 1397; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVVKVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDSTLDLDFKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
QY 121 KDLKSKSEPPRLFTPEEFRIFRNSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db 121 KDLKSKSEPPRLFTPEEFRIFRNSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSNSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWKRR 240
Db 181 KPFMLPVAASSLRNDSNSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWKRR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 2
US-08-628-428-9
; Sequence 9, Application US/08628428
; Patent No. 5885962
; GENERAL INFORMATION:
; APPLICANT: Lu, Hsieng
; TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,428
; FILING DATE: 05-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..273
; OTHER INFORMATION: 1-248 SCF protein begins at amino acid 26; amino acid 1-25
; OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
; OTHER INFORMATION: recombinant SCF."
US-08-628-428-9

Query Match 100.0%; Score 1397; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 2, 1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDVLPSCWISSEWVQSLDSTLDLDFKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
QY 61 MDVLPSCWISSEWVQSLDSTLDLDFKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120

Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
QY 121 KDLKSKSEPPRLFTPEEFRIFRNSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
Db 121 KDLKSKSEPPRLFTPEEFRIFRNSIDAFKDFVVASETSDCVSSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSNSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWKRR 240
Db 181 KPFMLPVAASSLRNDSNSSNRKAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWKRR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273
Db 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273

RESULT 3
US-08-482-918-49
; Sequence 49, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-49

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2, 1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNRYTNVVKVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDSTLDLDFKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120
Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKFSNISSEGLSNYSIIDLKLVNIYDVLVECKENSS 120

QY	181	KPMLPPVAASSLRDSSSNRKKNKPPGOSLTHAAMALPALFSLITGGFAGALYWKRR	240
Dd	181	KPMLPPVAASSLRDSSSNRKKNKPPGOSLTHAAMALPALFSLITGGFAGALYWKRR	240
QY	241	QPSLTAVENTIQINEDNEISMLOEKEREQEV	273
Dd	241	QPSLTAVENTIQINEDNEISMLOEKEREQEV	273
RESULT	5	US-09-224-681-49	

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RESULT 5
US-09-224-681-49
; Sequence 49, Application US/09224681
; Patent No. 6207454
;
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Sugars, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
;
; City: Chicago
;
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
;
INFORMATION FOR SEQ. ID NO.: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
;
TYPE: amino acid
STRANDEDNESS: single

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TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRTQWIIITCIIYDILLFNPVLTKEGICRNRVTNNVKDVTKLVAANLPKDYMITLKYPG 60
DB 1 MKRTQWIIITCIIYDILLFNPVLTKEGICRNRVTNNVKDVTKLVAANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVOLSDSLDLKFSNISSEGLSNYSIIDKLVINIVDDLVECKENSS 120
DB 61 MDVLPSCWISSEMYVOLSDSLDLKFSNISSEGLSNYSIIDKLVINIVDDLVECKENSS 120
QY 121 KDLKSKSPSPRLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVST 180
DB 121 KDLKSKSPSPRLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVST 180
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DB 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
QY 241 QPSLTRAIVENIQINEEDNEISMLQEKEREFQEV 273
DB 241 QPSLTRAIVENIQINEEDNEISMLQEKEREFQEV 273

RESULT 6

US-09-224-681-61
Sequence 61, Application US/09224681
Patent No. 6207454

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for enhancing the efficiency of gene transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA: 07/537,198
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-61

Query Match 100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRTQWIIITCIIYDILLFNPVLTKEGICRNRVTNNVKDVTKLVAANLPKDYMITLKYPG 60
DB 1 MKRTQWIIITCIIYDILLFNPVLTKEGICRNRVTNNVKDVTKLVAANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEMYVOLSDSLDLKFSNISSEGLSNYSIIDKLVINIVDDLVECKENSS 120
DB 61 MDVLPSCWISSEMYVOLSDSLDLKFSNISSEGLSNYSIIDKLVINIVDDLVECKENSS 120
QY 121 KDLKSKSPSPRLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVST 180
DB 121 KDLKSKSPSPRLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKDSRVST 180
QY 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
DB 181 KPFLPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLIIGFAGALYWKRR 240
QY 241 QPSLTRAIVENIQINEEDNEISMLQEKEREFQEV 273
DB 241 QPSLTRAIVENIQINEEDNEISMLQEKEREFQEV 273

RESULT 7

US-08-336-728A-48
Sequence 48, Application US/08336728A
Patent No. 6207802

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match          100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2,1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNVTNNVADYTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNVTNNVADYTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEMYVQVLSLTDLLDKFSNISGLSNYSIIDKLVIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMYVQVLSLTDLLDKFSNISGLSNYSIIDKLVIYVDLVECKENSS 120
QY 121 KDLKSEKSPERLFTPEEFRIENRSIDAFKDFVVAESDCCVSSSTLSPKDSRVSVT 180
DB 121 KDLKSEKSPERLFTPEEFRIENRSIDAFKDFVVAESDCCVSSSTLSPKDSRVSVT 180
QY 181 KPMLPPVAASSLRNDSSSSNRKAKNPPGDDSLHMAAALPALFSLITGFAGALYMKR 240
DB 181 KPMLPPVAASSLRNDSSSSNRKAKNPPGDDSLHMAAALPALFSLITGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273

RESULT 8
US-08-336-728A-49
Sequence 49, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: zsebo, Kristzina M.
APPLICANT: Bosseman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
```

```

ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-49

Query Match          100.0%; Score 1397; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 2,1e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNVTNNVADYTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYLOLLFNPVLTGEGICRNVTNNVADYTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEMYVQVLSLTDLLDKFSNISGLSNYSIIDKLVIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEMYVQVLSLTDLLDKFSNISGLSNYSIIDKLVIYVDLVECKENSS 120
QY 121 KDLKSEKSPERLFTPEEFRIENRSIDAFKDFVVAESDCCVSSSTLSPKDSRVSVT 180
DB 121 KDLKSEKSPERLFTPEEFRIENRSIDAFKDFVVAESDCCVSSSTLSPKDSRVSVT 180
QY 181 KPMLPPVAASSLRNDSSSSNRKAKNPPGDDSLHMAAALPALFSLITGFAGALYMKR 240
DB 181 KPMLPPVAASSLRNDSSSSNRKAKNPPGDDSLHMAAALPALFSLITGFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
DB 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFOEV 273
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Db 101 KPEMLPVAASSLRNDSSSSNRKAKNPBGSSSLHWPAMALPALFSLIIGFAGALYMKR 240
Qy 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
Db 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 11
US-09-224-681-48
Sequence 48, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseleman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match 99.6%; Score 1392; DB 4; Length 273;
Best Local Similarity 99.6%; Pred. No. 6,6e-134;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKKTQWIIITLCYIQLQLLENPVLTGTCRNRYTNVNVKDYTKLVANLPKDYITLKYVG 60
Db 1 MKKTQWIIITLCYIQLQLLENPVLTGTCICRNRYTNVNVKDYTKLVANLPKDYITLKYVG 60
Qy 61 MDVLPCHWISEMNVYVLSLFDLDPFNSISEGLSNYSITDKLVNVDLVECKENSS 120
Db 61 MDVLPCHWISEMNVYVLSLFDLDPFNSISEGLSNYSITDKLVNVDLVECKENSS 120
Qy 121 KDILKSEKSPERLFTPEEFRIFNRSIDAFKDFVASSETSCVYSTLSPEKDSRVST 180
Db 121 KDILKSEKSPERLFTPEEFRIFNRSIDAFKDFVASSETSCVYSTLSPEKDSRVST 180
Qy 181 KPEMLPVAASSLRNDSSSSNRKAKNPBGSSSLHMAAALPALFSLIIGFAGALYMKR 240
Db 181 KPEMLPVAASSLRNDSSSSNRKAKNPBGSSSLHWPAMALPALFSLIIGFAGALYMKR 240
Qy 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
Db 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 12
US-08-482-918-50
Sequence 50, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseleman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-50

Query Match 98.9%; Score 1381; DB 4; Length 273;

Best Local Similarity 98.9%; Pred. No. 8.8e-133;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVTEGICRNRVTNNVKDVTYKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVTEGICRNRVTNNVKDVTYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQVLSLTLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDKKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVYSTLSPEKDSRVSVT 180
DB 121 KDKKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVYSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAAPPDSSLHMAAMALPAFLSLIGFAFGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAAPPDSSLHMAAMALPAFLSLIGFAFGALYMKR 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREQEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREQEV 273

RESULT 13
US-09-224-681-50
Sequence 50, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: 104
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224, 681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005, 893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449, 653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982, 255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589, 701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573, 616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537, 198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/422, 383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36, 107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
SPRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-50

Query Match 98.9%; Score 1381; DB 4; Length 273;
Best Local Similarity 98.9%; Pred. No. 8.8e-133;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVTEGICRNRVTNNVKDVTYKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVTEGICRNRVTNNVKDVTYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLTLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQVLSLTLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
QY 121 KDKKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVYSTLSPEKDSRVSVT 180
DB 121 KDKKSFSPERLFTPEEFRIENRSIDAFKDFVAVSETSDCVYSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNRKAAPPDSSLHMAAMALPAFLSLIGFAFGALYMKR 240
DB 181 KPFMLPVAASSLRNDSSSNRKAAPPDSSLHMAAMALPAFLSLIGFAFGALYMKR 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREQEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREQEV 273

RESULT 14
US-08-336-728A-50
Sequence 50, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336, 728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:


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APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-50

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Query Match          98.6%; Score 1378; DB 4; Length 273;
Best Local Similarity 98.5%; Pred. No. 1.8e-132;
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKKTQWIIICITLLENNPLVKTGICRNVYNNKQVTVLVANLPKDYMITLKYYVG 60
Db 1 MKKTQWIIICITLLENNPLVKTGICRNVYNNKQVTVLVANLPKDYMITLKYYVG 60
QY 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
Db 61 MDVLPSCWISEMNVQVLSLTDLDKFSNISEGLSNYSIIDKLVNIYDDIVECKENSS 120
QY 121 KOLKSKFKPEPRLTPEEFRIENKSIDAFKDFVYVASETSDCVVSTLSPEKDSRVSVT 180
Db 121 KOLKSKFKPEPRLTPEEFRIENKSIDAFKDFVYVASETSDCVVSTLSPEKDSRVSVT 180
QY 181 KPFMLPVAASSLRNDSSSNKRNKPNPDSSSLHMAAALPALFSLIIGFAFAGALYMKR 240
Db 181 KPFMLPVAASSLRNDSSSNKRNKPNPDSSSLHMAAALPALFSLIIGFAFAGALYMKR 240
QY 241 QPSLTRAVENTIQINEDNEISMLOEKEREFOEV 273
Db 241 QPSLTRAVENTIQINEDNEISMLOEKEREFOEV 273

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RESULT 15
US-08-955-848A-82
Sequence 82, Application US/08955848A
Patent No. 5969105
GENERAL INFORMATION:
APPLICANT: Mc Welter, Charles
APPLICANT: Feng, Yiding
TITLE OF INVENTION: No. 5969105el Stem Cell Factor Receptor
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: G. D. Searle & Co.
STREET: P.O. Box 5110
CITY: Chicago
STATE: IL
COUNTRY: U. S. A.

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ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955, 848A
FILING DATE: 21-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,165
FILING DATE: 25-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2992/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-737-6986
TELEFAX: 314-737-6972
TELEX:
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-955-848A-82

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Query Match          90.6%; Score 1265; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-121;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 EGICRNRVTNNKQVTVKLVANLPKDYMITLKYYGMDVLPSCWISPMVQVLSLTDLD 85
Db 1 EGICRNRVTNNKQVTVKLVANLPKDYMITLKYYGMDVLPSCWISPMVQVLSLTDLD 85
QY 86 DKFSNISEGLSNYSIIDKLVNIYDDIVECKENSSKDLKSKFSPEPRLTPEEFRIEN 145
Db 61 DKFSNISEGLSNYSIIDKLVNIYDDIVECKENSSKDLKSKFSPEPRLTPEEFRIEN 120
QY 146 RSIDAFKDFVYVASETSDCVVSTLSPEKDSRVSVTKPFMLPVAASSLRNDSSSNKAK 205
Db 121 RSIDAFKDFVYVASETSDCVVSTLSPEKDSRVSVTKPFMLPVAASSLRNDSSSNKAK 180
QY 206 NPGDSSSLHMAAALPALFSLIIGFAFAGALYMKRQPSLTRAVENTIQINEDNEISMLOE 265
Db 181 NPGDSSSLHMAAALPALFSLIIGFAFAGALYMKRQPSLTRAVENTIQINEDNEISMLOE 240
QY 266 KEREFOEV 273
Db 241 KEREFOEV 248

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Search completed: August 18, 2002, 13:04:01
Job time: 166 sec

Sun Aug 18 14:09:03 2002

us-09-604-325a-61.rai

Page 10

1	1397	100.0	273	2	A35974	mast cell growth
2	1231	88.1	245	2	B61190	mast cell growth
3	1203.5	86.1	274	2	I46575	c-Kit ligand - piglet
4	1184.5	84.8	274	2	S47571	stem cell factor,
5	1180.5	84.5	274	2	I46929	stem cell factor,
6	1157	82.8	273	2	S65801	stem cell factor,
7	991	70.9	245	2	A37934	mast cell growth
8	885.5	63.4	202	2	S58313	mast cell growth
9	857	61.3	201	2	B35874	stem cell factor
10	703	50.3	287	2	JN0637	stem cell factor
11	702	50.3	287	2	S70366	stem cell factor
12	589	42.2	253	2	S70367	stem cell factor
13	576.5	41.3	124	2	S29052	stem cell factor
14	175.5	12.6	51	2	B35971	stem cell factor
15	172.5	12.3	49	2	A35971	stem cell factor
16	106	7.6	465	2	H97165	stem cell growth
17	101	7.2	1430	2	T16086	mast cell growth
18	100.5	7.2	402	2	T09062	flagellar hook-len
19	100.5	7.2	647	2	F90595	hypothetical protein
20	97.5	7.0	1107	2	S61667	probable advanced
21	97	6.9	1447	2	F82809	conserved hypothec
22	95.5	6.8	444	2	T25944	probable membrane
23	85.5	6.8	614	2	B86461	hypothetical protein
24	93.5	6.7	1293	2	T27886	hypothetical protein
25	92.5	6.7	1813	2	T19295	probable protein M
26	92.5	6.6	144	2	B69616	hypothetical protic
27	92.5	6.6	246	2	T19850	hypothetical prote
28	92.5	6.6	358	2	I53340	cell-division initi
29	92.5	6.6	512	2	G86773	hypothetical protel
						paired box transcr
						citrate (pro-35)-l

30	91.5	6.5	575	2	D84668	hypothetical prote
31	91.5	6.5	757	2	T18690	hypothetical prote
32	90.5	6.5	231	2	B86647	hypothetical prote
33	90.5	6.5	616	2	A69136	ATP-dependent Clp
34	90.5	6.5	1425	2	E89303	protein C47E8.8 [1
35	90.5	6.5	1675	2	T31473	hypothetical prote
36	90	6.4	774	2	F64300	formate dehydrogen
37	90	6.4	774	2	T32987	hypothetical prote
38	90	6.4	2100	2	T38128	t132.15 protein -
39	89.5	6.4	268	2	G81257	probable hemain up
40	89.5	6.4	335	2	S44922	K18 antigen - Enta
41	89.5	6.4	384	2	H64161	hypothetical prote
42	89	6.4	242	2	T27226	hypothetical prote
43	89	6.4	292	2	B71733	hypothetical prote
44	89	6.4	982	2	T15967	hypothetical prote
45	88.5	6.3	378	2	T25672	hypothetical prote

ALIGNMENTS

RESULT 1

mast cell growth factor precursor - human
N:Alternate names: kit ligand; stem cell factor
C:Species: Homo sapiens (man)

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C:\species: Homo sapiens (man)
C:\Data: 14-Dec-1000 #2222222
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c:/date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
C:/Accession: A3597A: A61190

R; Martin, F. H.: Suggs, S. V.

s, J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.T.; Wyrwch, I.; Sachdo

Cell 63, 203-211, 1990

A;Title: Primary structure and functional

A; Reference number: 137074

A;Accession: A35974
A:Molecule type: mRNA

A:Residues: 1-273 <MAB

A:Cross-references: GB:M599664: NTD:a3337933. PTDN:AAA85A50 1. PTD:a3337034

R;Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimbel, S.; Eisenman

Cell Growth Differ. 2, 373-378, 1991

A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and local

A;Reference number: A61190; MUID:92172791

A:Status: nucleic acid
A;Accession: Ab1190

A: Molecule type: mRNA
A: status: nucleic acid sequence not shown; not compared with conceptual translation

A:Residues: 1-273 <AND>

C;Genetics:

A;Gene: GDB:MGF

A;Cross-references: GDB:128

A;Map position: 12q22-12q22

Keywords: alternative splicing; extracellular matrix; mouse mast cell growth factor

Cysteine-rich; extracellular protein; glycoprotein; transmembrane F1-25/Domain: signal sequence #status predicted <SIG>

F;26-273/Product: mast cell growth factor #status predicted <MCS>

F;26-189/Product: (or 26-190) mast cell growth factor, soluble

Accession	Protein	Length	Weight	PI	Transmembrane	#status	predicted	<TMM>
F;215-237	Domain	21	215.237	4.5	1	1	1	1

E;90,97,118,145,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	100.0%	Score 1207	DB 2	12244 272
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	score	DB Z;	length
Best Local Similarity	100.08;	5.8e-103.	2/3,

Matches	273;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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0
cupps
0/
AUGUSTO
9/
0

0Y 1 MKKTQTWILTCIYLQLLFNPLVKTGICRNRVTNNVKDVTKLVANLPKDYMITLKYPG 6

[illegible]

DD 1 MKKIQIWLIIICLYLQLLLEFPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYYPG 6

QV 61 MDVLP SHCWTSEMVOI,SDSTJDI,DKFSNTSEGI SNKSTIDRI VNTYDNI VEGVIRENGC 1

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

Db 61 MDVLP SHCWISEM VVQLSDSLTDL DKFSNISEGLSNYSIIDKL VNIYDDLYECYKENS 1

1. *Chlorophyll a* (Chl *a*)

QY 121 KDLKKSFEKSPERLTPPEEFFRIENRSIDAFKDEVVASETSDCVSSTLSPEKDSRVSVT 1

[illegible]

OY 181 KPMLPVAASSLRNDSSSNRRKAKNPPGDSLSHMAAALPALFSLITIGFAGALYMKR 240
 |||||||
 DB 181 KPMLPVAASSLRNDSSSNRRKAKNPPGDSLSHMAAALPALFSLITIGFAGALYMKR 240
 |||||||
 OY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 |||||||
 DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 |||||||
 RESULT 2
 B61190
 mast cell growth factor, short form precursor - human
 N:Alternate names: kit ligand, short form; stem cell factor, short form
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
 C:Accession: B61190
 R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpe, S.; Eisenman, J.; Cannizzaro, I.
 Cell Growth Differ. 2, 373-376, 1991
 A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localize
 A:Reference number: A61190; MUID:92172791
 A:Accession: B61190
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-245 <AND>
 C:Comment: Alternative splicing produces this short form in which a predicted cleavage s
 C:Genetics:
 A:Gene: GDB:MCF
 A:Cross-references: GDB:128026; OMIM:184745
 A:Map position: 12q22-12q22
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: alternative splicing; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:187-209/Domain: transmembrane #status predicted <TM>
 F:90,97,118,145/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.1%; Score 1231; DB 2; Length 245;
 Best Local Similarity 89.4%; Pred. NO. 6.5e-90;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

OY 1 MKQTQWILTCIYQLLFNPLVTEGICRNRVTNNVKDYTKLVANLPKDYMITLKYVG 60
 |||||||
 DB 1 MKQTQWILTCIYQLLFNPLVTEGICRNRVTNNVKDYTKLVANLPKDYMITLKYVG 60
 |||||||
 OY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISSEGLSNYSITDKLVNIVDVLVECVKENS 120
 |||||||
 DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISSEGLSNYSITDKLVNIVDVLVECVKENS 120
 |||||||
 OY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSITLSPKDSRVSV 180
 |||||||
 DB 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSITLSPKDSRVSV 180
 |||||||
 OY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSITLSPKDSRVSV 180
 |||||||
 DB 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSITLSPKDSRVSV 180
 |||||||
 OY 181 KPMLPVAASSLRNDSSSNRRKAKNPPGDSLSHMAAALPALFSLITIGFAGALYMKR 240
 |||||||
 DB 181 KPMLPVAASSLRNDSSSNRRKAKNPPGDSLSHMAAALPALFSLITIGFAGALYMKR 240
 |||||||
 OY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 |||||||
 DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 |||||||
 RESULT 3
 146575
 c-kit ligand - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: 146575
 R:Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
 A:Reference number: 146575; MUID:94146218
 A:Accession: 146575

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHA>
 A:Cross-references: GB:107786; NID:g164420; PIDN:AAA53670.1; PID:g164421
 C:Superfamily: mouse mast cell growth factor

Query Match 86.1%; Score 1203.5; DB 2; Length 274;
 Best Local Similarity 85.8%; Pred. NO. 1.1e-87;
 Matches 235; Conservative 22; Mismatches 16; Indels 1; Gaps 1;

OY 1 MKQTQWILTCIYQLLFNPLVTEGICRNRVTNNVKDYTKLVANLPKDYMITLKYVG 60
 |||||||
 DB 1 MKQTQWILTCIYQLLFNPLVTEGICRNRVTNNVKDYTKLVANLPKDYMITLKYVG 60
 |||||||
 OY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISSEGLSNYSITDKLVNIVDVLVECVKENS 120
 |||||||
 DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISSEGLSNYSITDKLVNIVDVLVECVKENS 120
 |||||||
 OY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSITLSPKDSRVSV 179
 |||||||
 DB 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSITLSPKDSRVSV 180
 |||||||
 OY 180 TKPFMLPVAASSLRNDSSSNRRKAKNPPGDSLSHMAAALPALFSLITIGFAGALYMKR 239
 |||||||
 DB 181 TKPFMLPVAASSLRNDSSSNRRKAKNPPGDSLSHMAAALPALFSLITIGFAGALYMKR 240
 |||||||
 OY 240 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 |||||||
 DB 241 KQNLTRFVENVIOINEDNEISMLOEKEREFOEV 274
 |||||||
 RESULT 4
 S47571
 stem cell factor, longer isoform - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S47571
 R:Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
 Blochim. Biophys. Acta 1223, 148-150, 1994
 A:Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine
 A:Reference number: S47571; MUID:94339176
 A:Accession: S47571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHO>
 A:Cross-references: EMBL:D28934; NID:g538520; PIDN:BA06061.1; PID:g538521
 C:Superfamily: mouse mast cell growth factor

Query Match 84.8%; Score 1184.5; DB 2; Length 274;
 Best Local Similarity 84.7%; Pred. NO. 3.5e-86;
 Matches 232; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

OY 1 MKQTQWILTCIYQLLFNPLVTEGICRNRVTNNVKDYTKLVANLPKDYMITLKYVG 60
 |||||||
 DB 1 MKQTQWILTCIYQLLFNPLVTEGICRNRVTNNVKDYTKLVANLPKDYMITLKYVG 60
 |||||||
 OY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISSEGLSNYSITDKLVNIVDVLVECVKENS 120
 |||||||
 DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISSEGLSNYSITDKLVNIVDVLVECVKENS 120
 |||||||
 OY 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSITLSPKDSRVSV 179
 |||||||
 DB 121 KDLKSFSPERLFTPEEFRIENRSIDAFKDFVVASETSDCVVSSITLSPKDSRVSV 180
 |||||||
 OY 180 TKPFMLPVAASSLRNDSSSNRRKAKNPPGDSLSHMAAALPALFSLITIGFAGALYMKR 239
 |||||||
 DB 181 TKPFMLPVAASSLRNDSSSNRRKAKNPPGDSLSHMAAALPALFSLITIGFAGALYMKR 240
 |||||||
 OY 240 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 |||||||
 DB 241 KQNLTRFVENVIOINEDNEISMLOEKEREFOEV 274
 |||||||

RESULT 5
 146929
 C:Species: Canis lupus familiaris (dog)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
 C:Accession: 146929
 R:Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
 Exp. Hematol. 20, 118-124, 1992
 A:Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic F
 A:Reference number: 146929; MUID:93106145
 A:Accession: 146929
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-274 <SHU>
 A:Cross-references: GB:S53329; NID:g262240; PIDN:AA824619.1; PID:g262241
 C:Superfamily: mouse mast cell growth factor

Query Match 84.5%; Score 1180.5; DB 2; Length 274;
 Best Local Similarity 85.4%; Pred. No. 7.3e-86;
 Matches 234; Conservative 17; Mismatches 22; Indels 1; Gaps 1;
 QY 1 MKKTQTWITTCYIQLLLFNPVLTGEGICRRVYNNVADVKLVANLPKDYMTLKYVPG 60
 Db 1 MKKTQTWITTCYIQLLLFNPVLTGEGICRRVYNNVADVKLVANLPKDYMTLKYVPG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLTLDDKFSNISEGLSNYSIIDKLVNIVDDVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQLSDSLTLDDKFSNISEGLSNYSIIDKLVNIVDDVECKENSS 120
 QY 121 KDLKSEKSPERLFTPEEFRRINRSIDAFKDF-VVASETSDCVSSTLSPKDSRSV 179
 Db 121 ENVKAPKSPERLFTPEEFRRINRSIDAFKDFETVASKSECVSSTLSPKDSRSV 180
 QY 180 TKPFLPVAASLRNDSNRRKAKNPQDSSLHMAALPALFSLIGFAGALYWK 239
 Db 181 TKPFLPVAASLRNDSNRRKAKNPQDSSLHMAALPALFSLIGFAGALYWK 240
 QY 240 KQPSLTRAVENTIQINEDNEISMLQEKREPOEV 273
 Db 241 KQPSLTRAVENTIQINEDNEISMLQEKREPOEV 274

RESULT 6
 563801
 mast cell growth factor - mouse
 N:Alternate names: hematopoietic growth factor KL; ligand steel factor; stem cell factor
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000
 C:Accession: S65801; A43751; A35976; A35977; A35972; A35975; A35973; I48768
 R:Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
 Genetics 142, 927-934, 1996
 A:Title: Multiple pathways for Steel regulation suggested by genomic and sequence analysis
 A:Reference number: S65801; MUID:97002551
 A:Accession: S65801
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-273 <BED>
 A:Cross-references: EMBL:U44725; NID:g1172215; PIDN:AA652447.1; PID:g1172216
 R:Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A:Title: Differential expression and processing of two cell associated forms of the kit-
 A:Reference number: A43751; MUID:92330001
 A:Accession: A43751
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-214, 'V', 216-273 <HUA>
 A:Cross-references: GB:S40364; NID:g251668; PIDN:AA822554.2; PID:g5705957
 R:Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Leder
 Cell 63, 225-233, 1990

A:Title: The hematopoietic growth factor KL is encoded by the S1 locus and is the lig
 A:Reference number: A35976; MUID:91004221
 A:Accession: A35976
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-206, 'S', 208-270 <HU2>
 A:Cross-references: GB:M38511
 R:Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; Mar
 Cell 63, 235-243, 1990
 A:Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active
 A:Reference number: A35977; MUID:91004223
 A:Accession: A35977
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-273 <AND>
 A:Cross-references: GB:M57647; GB:M38436; NID:g199151; PIDN:AA39538.1; PID:g199152
 R:Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.;
 Cell 63, 175-183, 1990
 A:Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and
 A:Reference number: A35972; MUID:91004216
 A:Accession: A35972
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 26-53 <COP>
 A:Cross-references: GB:M59912
 R:Csebo, K.M.; Williams, D.A.; Geissler, E.N.; Broudy, V.C.; Martin, F.H.; Atkins, H.
 Cell 63, 213-224, 1990
 A:Title: Stem cell factor is encoded at the S1 locus of the mouse and is the ligand f
 A:Reference number: A35975; MUID:91004220
 A:Accession: A35975
 A:Molecule type: mRNA
 A:Residues: 1-201 <ZSE>
 A:Cross-references: GB:M59915; NID:g200935; PIDN:AAA40095.1; PID:g554271
 R:Csebo, K.M.; Wypych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachd
 A.; Langley, K.E.
 Cell 63, 195-201, 1990
 A:Title: Identification, purification, and biological characterization of hematopiet
 A:Reference number: A35973; MUID:91004218
 A:Accession: A35973
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-29, 'R', 31-39 <ZS2>
 R:Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.
 Genes Dev. 6, 1832-1842, 1992
 A:Title: Developmental abnormalities in Steel17H mice result from a splicing defect 1
 A:Reference number: A44071; MUID:93012940
 A:Accession: 148768
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-206, 'S', 208-273 <RES>
 A:Cross-references: EMBL:X68989; NID:g395283; PIDN:CAA48778.1; PID:g395284
 C:Genetics:
 A:Gene: SLF
 A:Map position: 10
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: extracellular protein; glycoprotein; transmembrane protein

Query Match 82.8%; Score 1157; DB 2; Length 273;
 Best Local Similarity 82.8%; Pred. No. 5.2e-84;
 Matches 226; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
 QY 1 MKKTQTWITTCYIQLLLFNPVLTGEGICRRVYNNVADVKLVANLPKDYMTLKYVPG 60
 Db 1 MKKTQTWITTCYIQLLLFNPVLTGEGICRRVYNNVADVKLVANLPKDYMTLKYVPG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLTLDDKFSNISEGLSNYSIIDKLVNIVDDVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQLSDSLTLDDKFSNISEGLSNYSIIDKLVNIVDDVECKENSS 120
 QY 121 KDLKSEKSPERLFTPEEFRRINRSIDAFKDFVVASETSDCVSSTLSPKDSRSV 180
 Db 121 KDLKSEKSPERLFTPEEFRRINRSIDAFKDFVVASETSDCVSSTLSPKDSRSV 180

Db 121 KNIKSPKRPETRTSTPEEFISINRSIDAFKDNVAVSDTSDCVLSTLGPCKDSRVSVT 180
 Qy 181 KPFLPVPVAASSLRNDSSSSNNKAKNPDPGSSLSHMAAMALPALPSLITGFAFGALYWKRR 240
 Db 181 KPFLPVPVAASSLRNDSSSSNNKAKNPDPGSSLSHMAAMALPALPSLITGFAFGALYWKRR 240
 Qy 241 OPSTRAVENIQTINEDNEISMLOEKERPEFQEV 273
 Db 241 OPSTRAVENIQTINEDNEISMLOEKERPEFQEV 273

RESULT 7

best cell growth factor precursor (version 2) - mouse

N:Alternate names: KL-2 protein

C:Species: Mus musculus (house mouse)

C>Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000

C:Accession: A37934; B43751

R:Flanagan, J.G.; Chan, D.C.; Leder, P.

Cell 64, 1035-1035, 1991

A:Title: Transmembrane form of the kit ligand growth factor is determined by alternative

A:Reference number: A37934; MUID:91160046

A:Accession: A37934

A:Molecule type: mRNA

A:Residues: 1-245 <FLA>

A:Cross-references: GB:M64262

R:Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.

Mol. Biol. Cell 3, 349-362, 1992

A:Title: Differential expression and processing of two cell associated forms of the kit-

A:Reference number: A43751; MUID:92330001

A:Accession: B43751

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-173, 'R', '175-186, 'L', '188-245 <HUA>

A:Cross-references: GB:S04534

A:Note: the authors translated the codon TTG for residue 187 as Trp

C:Superfamily: mouse mast cell growth factor

Query Match

Best local Similarity 70.9%; Score 991; DB 2; Length 245;

Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

Qy 1 MKKTQWILTCIYQLLFPNPKTEGICRNRVNNKQVTKLVANLPKDMITLKYVPG 60
 Db 1 MKKTQWILTCIYQLLFPNPKTEGICRNRVNNKQVTKLVANLPKDMITLKYVAG 60
 Qy 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIDKLKIVDVLVCEKENS 120
 Db 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIDKLKIVDVLVCEKENS 120
 Qy 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
 Db 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
 Qy 181 KPFLPVPVAASSLRNDSSSSNNKAKNPDPGSSLSHMAAMALPALPSLITGFAFGALYWKRR 240
 Db 181 KPFLPVPVAASSLRNDSSSSNNKAKNPDPGSSLSHMAAMALPALPSLITGFAFGALYWKRR 240
 Qy 241 OPSTRAVENIQTINEDNEISMLOEKERPEFQEV 273
 Db 241 OPSTRAVENIQTINEDNEISMLOEKERPEFQEV 273

RESULT 8

stem cell factor precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000

C:Accession: S58313

R:Minnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.

submitted to the EMBL Data Library, August 1995

A:Description: Molecular cloning and biological activity of ovine stem cell factor.

A:Reference number: S58313
 A:Accession: S58313
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-202 <MCIG>
 A:Cross-references: EMBL:250743; NID:940807; PIDN:CAA90620.1; PID:940808
 C:Superfamily: mouse mast cell growth factor

Query Match

Best local Similarity 63.4%; Score 885.5; DB 2; Length 202;

Matches 174; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MKKTQWILTCIYQLLFPNPKTEGICRNRVNNKQVTKLVANLPKDMITLKYVPG 60
 Db 1 MKKTQWILTCIYQLLFPNPKTEGICRNRVNNKQVTKLVANLPKDMITLKYVAG 60
 Qy 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIDKLKIVDVLVCEKENS 120
 Db 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIDKLKIVDVLVCEKENS 120
 Qy 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 179
 Db 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
 Qy 180 TKPFLPVPVAASSLRNDSSSSN 201
 Db 181 TKPFLPVPVAASSLRNDSSSSN 202

RESULT 9

stem cell factor protein precursor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000

C:Accession: B35974; A39805

R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, S.J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev

Cell 63, 203-211, 1990

A:Title: Primary structure and functional expression of rat and human stem cell facto

A:Reference number: A35974; MUID:91004219

A:Accession: B35974

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-201 <MAR>

A:Cross-references: GB:M59966; NID:9206661; PIDN:AAA2117.1; PID:9554507

R:Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zse

J. Biol. Chem. 266, 8102-8107, 1991

A:Title: Amino acid sequence and post-translational modification of stem cell factor

A:Reference number: A39805; MUID:91217037

A:Accession: A39805

A:Status: preliminary

A:Molecule type: protein

A:Residues: 'E', '27-190 <LUA>

C:Superfamily: mouse mast cell growth factor

Query Match

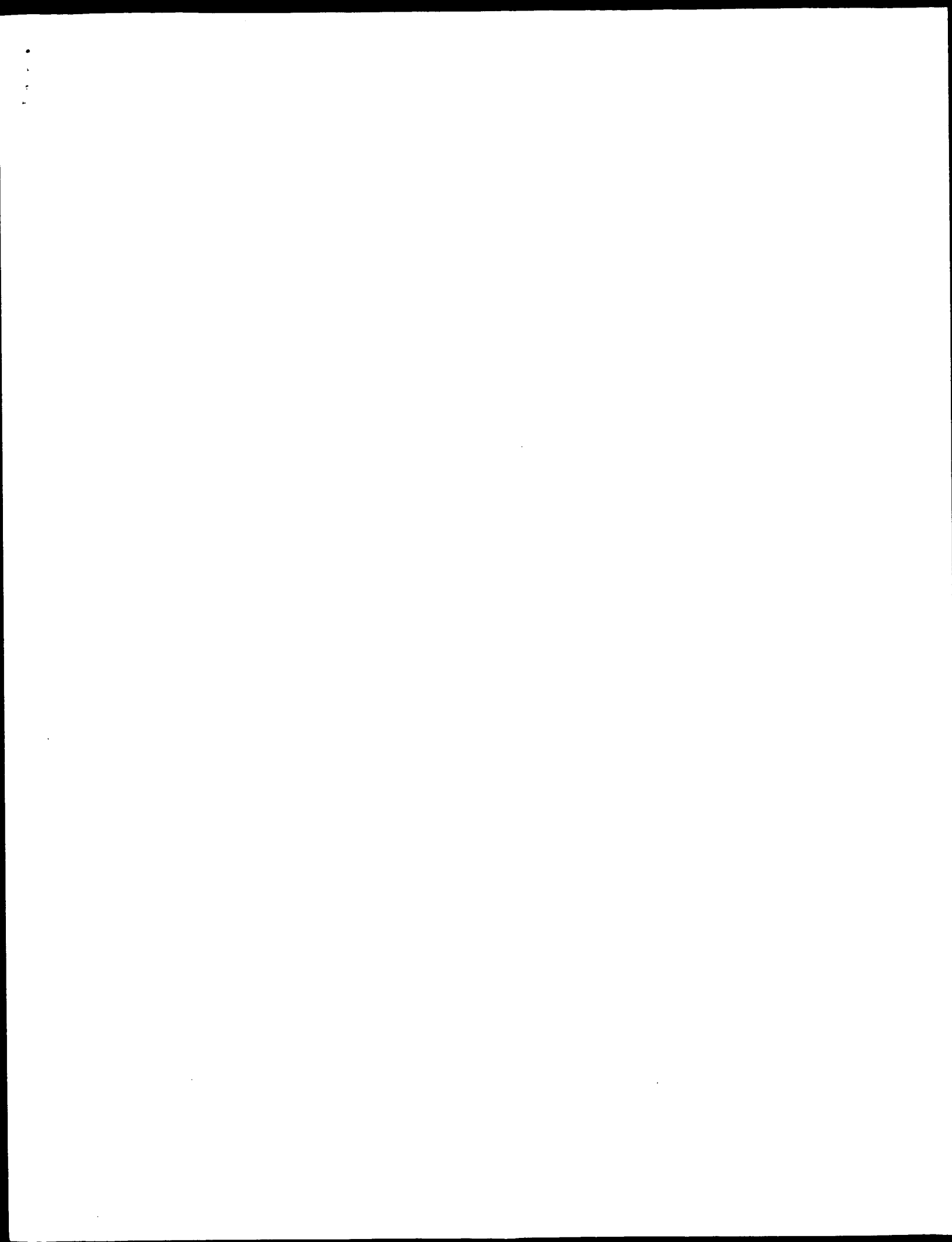
Best local Similarity 61.3%; Score 857; DB 2; Length 201;

Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MKKTQWILTCIYQLLFPNPKTEGICRNRVNNKQVTKLVANLPKDMITLKYVPG 60
 Db 1 MKKTQWILTCIYQLLFPNPKTEGICRNRVNNKQVTKLVANLPKDMITLKYVAG 60
 Qy 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIDKLKIVDVLVCEKENS 120
 Db 61 MDVLPSCWISSEMYVQSLDLDLDFKSNISGLSNYSIDKLKIVDVLVCEKENS 120
 Qy 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180
 Db 121 KDLKSKSPERLFTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPKDSRVSVT 180

Sun Aug 18 14:09:04 2002

us-09-604-325a-61.rpt



Accession	Length	Score	Ident	Model	Species
33	86	6.2	399	1	PX8D_HUMAN
33	86	6.2	399	1	Q09155 homo sapien

FT	DOMAIN	238	273	CYTOPLASMIC (P)
FT	DOMAIN	238	273	CYTOPLASMIC (P)

FT DISULFID 29 114 BY SIMILARITY.

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FT DISULFID 68 163 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ CARBOHYD 273 AA; 30898 MW; 19FD362CB59C6607 CRC64;

Query Match 100.0%; Score 1397; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8e-101;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWITTCIYQLLFNPLVKTBEICRRNRYNNKYTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWITTCIYQLLFNPLVKTBEICRRNRYNNKYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCHWISEMVOVLSLTDLDKFSNISEGLSNYSIIDKLVNIYDDLVCEVKENS 120
DB 61 MDVLPSCHWISEMVOVLSLTDLDKFSNISEGLSNYSIIDKLVNIYDDLVCEVKENS 120
QY 121 KDLKSEKSPPEPLFTPEEFRIFNRSIDAFKDFVAVASETSDCVYSTLSPEKDSRVSVT 180
DB 121 KDLKSEKSPPEPLFTPEEFRIFNRSIDAFKDFVAVASETSDCVYSTLSPEKDSRVSVT 180
QY 181 KPFMLPPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLITIGFAGALYMKR 240
DB 181 KPFMLPPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLITIGFAGALYMKR 240
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREPOEV 273
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREPOEV 273

RESULT 2
SCF_PIG 2
ID SCF_PIG STANDARD; PRT: 274 AA.
AC 029030:
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
  cell growth factor) (MGF).
DE KITLG OR MGF.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RX MEDLINE=94146218; PubMed=7508758;
  Zhang Z., Anthony R.V.;
  "Porcine stem cell factor/c-kit ligand: its molecular cloning and
  localization within the uterus.";
  Biol. Reprod. 50:95-102(1994).
CC -I- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
  AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
  HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
  CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
  PROBABLY INTERLEUKINS (BY SIMILARITY).
CC -I- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
  SECRETED SOLUBLE FORM.
CC -I- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC EMBL: L0786; AAA53670.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 274 KIT LIGAND.
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 POTENTIAL.
FT DISULFID 29 114 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 239 274 BY SIMILARITY.
FT CARBOHYD 68 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ CARBOHYD 274 AA; 31118 MW; F93C8711AD7BA6A6 CRC64;

Query Match 86.1%; Score 1203.5; DB 1; Length 274;
Best Local Similarity 85.8%; Pred. No. 2.7e-86;
Matches 235; Conservative 22; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKKTQWITTCIYQLLFNPLVKTBEICRRNRYNNKYTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWITTCIYQLLFNPLVKTBEICRRNRYNNKYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCHWISEMVOVLSLTDLDKFSNISEGLSNYSIIDKLVNIYDDLVCEVKENS 120
DB 61 MDVLPSCHWISEMVOVLSLTDLDKFSNISEGLSNYSIIDKLVNIYDDLVCEVKENS 120
QY 121 KDLKSEKSPPEPLFTPEEFRIFNRSIDAFKDFVAVASETSDCVYSTLSPEKDSRVSVT 179
DB 121 KDLKSEKSPPEPLFTPEEFRIFNRSIDAFKDFVAVASETSDCVYSTLSPEKDSRVSVT 180
QY 180 TKPFMLPPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLITIGFAGALYMKR 239
DB 180 TKPFMLPPVAASSLRNDSSSNRKAKNPPGDSLHMAAMALPALFSLITIGFAGALYMKR 240
QY 240 ROPSLTRAVENTIOINEDNEISMLOEKEREPOEV 273
DB 240 ROPSLTRAVENTIOINEDNEISMLOEKEREPOEV 274

RESULT 3
SCF_CANFA 3
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AC 006220:
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
  cell growth factor) (MGF).
DE KITLG OR MGF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93106145; PubMed=1281786;
  Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W.,
  Martin F.H.;
  "Canine stem cell factor (c-kit ligand) supports the survival of
  hematopoietic progenitors in long-term canine marrow culture.";
  Exp. Hematol. 20:1118-1124(1992).
CC -I- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
  AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
  HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
  CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
  PROBABLY INTERLEUKINS.
CC -I- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).

```

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 DR EMBL: S53329; AAB24619.1; -
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25
 FT CHAIN 1 25
 FT DOMAIN 26 274
 FT DOMAIN 26 215
 FT TRANSMEM 216 238
 FT DOMAIN 239 274
 FT DISULFID 29 114
 FT DISULFID 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 FT SEQUENCE 274 AA; 30869 MW; 4182B9AED00793B CRC64;
 Query Match 84.5%; Score 1180.5; DB 1; Length 274;
 Best Local Similarity 85.4%; Pred. No. 1.6e-84;
 Matches 234; Conservative 17; Mismatches 22; Indels 1; Gaps 1;
 QY 1 MKKTQWILNCIYLIQLLEPLVKTBCICNRRTNWKVTKLVANLPKDYMTLTKYVPG 60
 DB 1 MKKTQWILNCIYLIQLLEPLVKTBCICNRRTNWKVTKLVANLPKDYMTLTKYVPG 60
 QY 61 MDVLPSCWISWVYVQSLDLDLDFSNISGLSNYSITDKLVNIVDDLYECVKNSS 120
 DB 61 MDVLPSCWISWVYVQSLDLDLDFSNISGLSNYSITDKLVNIVDDLYECVKNSS 120
 QY 121 KDLAKSKSPKPEPLTPPEEFRRFNRSIDAKDF-VVASETSDCVVSTLSPEKDSRVSY 179
 DB 121 ENVKKAPKSPKPEPLTPPEEFRRFNRSIDAKDFVAVASETSDCVVSTLSPEKDSRVSY 180
 QY 180 TKPFMLPPVAASSLRDSSSNKAKNPQDSSLHMAALPALFSLIIGFAFALYMKK 239
 DB 181 TKPFMLPPVAASSLRDSSSNKAKNSIGDSMLQMAALPALFSLVIGFAFALYMKK 240
 QY 240 RQPSLTRAVENTIQINEDNEISMLQEKEREFOEV 273
 DB 241 KQPNLTRVETNIQINEDNEISMLQEKEREFOEV 274
 RESULT 4
 SCF_MOUSE STANDARD: PRT: 273 AA.
 ID SCF_MOUSE
 AC P20826;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGF) (Hematopoietic growth factor KL) (KL-1
 DE protein) (Steel factor).
 GN KITLG OR KITL OR MGF OR SL OR SLF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-MC6BF1;
 RX MEDLINE=91004223; PubMed=1698558;
 RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
 RA Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D.,
 RA Williams D.E.;
 RT "Molecular cloning of mast cell growth factor, a hematopoietin that
 RT is active in both membrane bound and soluble forms.";
 RL Cell 63:235-243(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92330001; PubMed=1378327;
 RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
 RT "Differential expression and processing of two cell associated forms
 RT of the kit-ligand: KL-1 and KL-2.";
 RL Mol. Biol. Cell 3:349-362(1992).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-MC6BF1;
 RX MEDLINE=91160046; PubMed=1705866;
 RA Flanagan J.G., Chan D.C., Leder P.;
 RT "Transmembrane form of the kit ligand growth factor is determined by
 RT alternative splicing and is missing in the sld mutant.";
 RL Cell 64:1025-1035(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93012940; PubMed=1383087;
 RA Brannan C.T., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
 RA Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A.,
 RA Copeland N.G.;
 RT "Developmental abnormalities in Steel17H mice result from a splicing
 RT defect in the steel factor cytoplasmic tail.";
 RL Genes Dev. 6:1832-1842(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97002551; PubMed=8849898;
 RA Bedell M.A., Copeland N.G., Jenkins N.A.;
 RT "Multiple pathways for steel regulation suggested by genomic and
 RT sequence analysis of the murine steel gene.";
 RL Genetics 142:927-934(1996).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=(102/ELX3H/EL)F1; TISSUE=Brain;
 RA Gray J.;
 RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 1-270 FROM N.A., AND SEQUENCE OF 26-65.
 RX MEDLINE=91004221; PubMed=1698557;
 RA Huang E., Nocka K., Beller D.R., Chu T.Y., Buck J., Lahm H.W.,
 RA Wellner D., Leder P., Besmer P.;
 RT "The hematopoietic growth factor KL is encoded by the sl locus and is
 RT the ligand of the c-kit receptor, the gene product of the w locus.";
 RL Cell 63:225-233(1990).
 RN [8]
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zsebo K.M., Williams D.A., Geissler E.N., Broudy V.C., Martin F.H.,
 RA Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Murodock D.C.,
 RA Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattaneach B.M.,
 RA Galli S.J., Suggs S.V.;
 RT "Stem cell factor is encoded at the sl locus of the mouse and is the
 RT ligand for the c-kit tyrosine kinase receptor.";
 RL Cell 63:213-224(1990).
 RN [9]
 RP SEQUENCE OF 26-53.
 RX MEDLINE=91004216; PubMed=1698554;
 RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.;
 RT "Mast cell growth factor maps near the steel locus on mouse
 RT chromosome 10 and is deleted in a number of steel alleles.";
 RL Cell 63:175-183(1990).
 RN [10]
 RP PARTIAL SEQUENCE OF 26-78.

RX MEDLINE=91004215; Pubmed=1698553;
 RA Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K.,
 RA March C.J., Park L.S., Martin U., Mochizuki D.Y., Roswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.;
 RT "Identification of a ligand for the c-kit proto-oncogene";
 RL Cell 63:167-174(1990).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVELY SPLICED FORMS DIFFERING BY
 CC THE PRESENCE OR ABSENCE OF EXON 6 HAVE BEEN OBSERVED AND OCCUR IN
 CC VARYING RATIOS IN DIFFERENT TISSUES.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PM: THE LONG FORM APPEARS TO CONTAIN A PROTEOLYTIC CLEAVAGE SITE
 CC ENCODED BY EXON 6 SUCH THAT THE ACTIVE REGION OF THE EXTRACELLULAR
 CC DOMAIN IS RELEASED FROM THE MEMBRANE IN A SOLUBLE FORM.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: M59915; AAA40095.1; -;
 CC DR EMBL: M57647; AAA39538.1; -;
 CC DR EMBL: X68889; CAA48778.1; -;
 CC DR EMBL: U44724; -; NOT_ANNOTATED_CDS.
 CC DR EMBL: U44725; AAC52447.1; -;
 CC DR EMBL: X95381; CAA64667.1; -;
 CC DR EMBL: S40364; AAB22554.2; -;
 CC DR EMBL: M59912; AAA39539.1; -;
 CC DR PIR: A35971; A35971.
 CC DR PIR: A35972; A35972.
 CC DR PIR: A35975; A35975.
 CC DR PIR: A35976; A35976.
 CC DR PIR: A35977; A35977.
 CC DR PIR: A43751; A43751.
 CC DR PIR: B35971; B35971.
 CC DR MGI: 96974; Kiti.
 CC DR InterPro: IPR003452; SCF.
 CC DR Pfam: PF02404; SCF; 1.
 CC KW Growth factor; Glycoprotein; Transmembrane; Signal;
 CC KW Alternative splicing; Cell adhesion.
 CC FT SIGNAL 1 25
 CC FT CHAIN 26 273 KIT LIGAND.
 CC FT DOMAIN 26 214 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 215 237 POTENTIAL.
 CC FT DOMAIN 238 273 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 29 114 BY SIMILARITY.
 CC FT CARBOHYD 68 163 BY SIMILARITY.
 CC FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPPLIC 175 202 MISSING (IN SOLUBLE ISOFORM).
 CC FT VARIANT 207 207 A -> S.
 CC FT CONFLICT 215 215 W -> L (IN REF. 2).
 CC SQ SEQUENCE 273 AA; 30645 MW; A7FC89B592A7967 CMC64;

Query Match 82.8%; Score 1157; DB 1; Length 273;
 Best local Similarity 82.8%; Pred. No. 1.1e-82;
 Matches 226; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
 1 MKKTQWITTCIYIOLLFLNPLVKTEIGCRNRYNNVADYTLVAMLRDRIITIKYYPG 60

DB 1 MKKTQWITTCIYIOLLFLNPLVKTEIGCRNRYNNVADYTLVAMLRDRIITIKYYPG 60
 QY 61 MDVLPSCHEISEMYYVOLDSLTDLDRKFSNISEGLSNISIDKLVNIYDDIYECYKEMSS 120
 DB 61 MDVLPSCHEISEMYYVOLDSLTDLDRKFSNISEGLSNISIDKLVNIYDDIYECYKEMSS 120
 QY 121 KOLKFSKSPEDRLPPEEFRIENRSDAFKDFVASTSCVASTLSPKDSRSVST 180
 DB 121 KNKESPKRPERSPFEEFISFNISDAFDVASTSDSCVASTLSPKDSRSVST 180
 QY 181 KPEMLPVAASSLRNDSSSNRRKANPDDSLHMAAMLPALFSLIIGFAGALYMKR 240
 DB 181 KPEMLPVAASSLRNDSSSNRRKANPDDSLHMAAMLPALFSLIIGFAGALYMKR 240
 QY 241 QPSLTRAVENTIQINEDNISMLOEKEREFOY 273
 DB 241 QPSLTRAVENTIQINEDNISMLOEKEREFOY 273
 RESULT 5
 SCF_RAT STANDARD; PRT; 201 AA.
 ID SCF_RAT
 AC P21581;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
 DE cell growth factor) (Mgf) (Fragment).
 GN KITLG OR MGf.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP MEDLINE=91004215; Pubmed=2208279;
 RA Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Tung J., Okino K.H.,
 RA Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
 RA Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
 RA Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J.C., Sachdev R.K.,
 RA Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
 RT "Primary structure and functional expression of rat and human stem
 RT cell factor DNAs";
 RL Cell 63:203-211(1990).
 RN [2]
 RP SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RC STRAIN=BUFALO; TISSUE=Liver;
 RX MEDLINE=91217037; Pubmed=1708771;
 RA Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
 RA Mendiaz E.A., Zsebo K.M., Langley K.E.;
 RT "Amino acid sequence and post-translational modification of stem cell
 RT factor isolated from buffalo rat liver cell-conditioned medium";
 RL J Biol. Chem. 266:8102-8107(1991).
 RN [3]
 RP SEQUENCE OF 26-39.
 RX MEDLINE=91004218; Pubmed=2208278;
 RA Zsebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A.,
 RA Karkare S.B., Sachdev R.K., Yuschenko V.N., Birkett N.C.,
 RA Williams L.R., Satyagal V.N., Tung W., Bosseman R.A., Mendiaz E.A.,
 RA Langley K.E.;
 RT "Identification, purification, and biological characterization of
 RT hematopoietic stem cell factor from buffalo rat liver-conditioned
 RT medium";
 RL Cell 63:195-201(1990).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.

CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -----
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 CC -----
 CC EMBL: M59966; AAA42117.1; -
 CC PIR: B35974; B35974.
 CC DR PIR: A35973; A35973.
 CC DR InterPro: IPR003452; SCF.
 CC DR Pfam: PF02404; SCF, 1.
 CC KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 CC FT SIGNAL 1 25
 CC FT CHAIN 26 >201
 CC FT MOD_RES 26 26
 CC FT DISULFID 29 114
 CC FT DISULFID 68 163
 CC FT CARBOHYD 90 90
 CC FT CARBOHYD 145 145
 CC FT CARBOHYD 167 167
 CC FT CARBOHYD 168 168
 CC FT CARBOHYD 180 180
 CC FT CARBOHYD 195 195
 CC FT NON_TER 201
 CC SQ SEQUENCE 201 AA; 22537 MW; 188868C1DAF271B CRC64;
 Query Match 61.3%; Score 857; DB 1; Length 201;
 Best Local Similarity 82.6%; Pred. No. 1.2e-59;
 Matches 166; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MKKQTWILTCIYQLLEFNPVKTGICRNRYNNKVDKLVANIPKRYMTITLKYVG 60
 Db 1 MKKQTWILTCIYQLLEFNPVKTGICRNRYNNKVDKLVANIPKRYMTITLKYVG 60
 QY 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSISGLSNYSIIDKLIVNIVDLVECKENS 120
 Db 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSISGLSNYSIIDKLIVNIVDLVECKENS 120
 QY 121 KDLKSKSEPPRLTPEEPFRIFNRSIDAFKPVVAASETSCVVSSTLSPEKDSRYVT 180
 Db 121 KVKKESLAKKETKFTPEEFISIFNRSIDAFKDFVWASDTSCVLSSTLGEKDSRYVT 180
 QY 181 KPFMLPVAASSLRNDSSSN 201
 Db 181 KPFMLPVAASSLRNDSSSN 201
 RESULT 6
 SCF_CHICK 6
 ID SCF_CHICK STANDARD; PRT; 287 AA.
 AC 009108;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGF).
 GN KITLG.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN 11
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9373244; PubMed=7684722;
 RX Zhou J., Ohlaki M., Sakurai M.;
 RT "Sequence of a cDNA encoding chicken stem cell factor.";
 RL Gene 127:269-270(1993).

CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC -----
 CC EMBL: D13516; BAA02733.1; -
 CC PIR: JN0637; JN0637.
 CC DR PIR: JN0637; JN0637.
 CC DR InterPro: IPR003452; SCF.
 CC DR Pfam: PF02404; SCF, 1.
 CC KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 CC FT SIGNAL 1 25
 CC FT CHAIN 26 287
 CC FT DOMAIN 26 225
 CC FT TRANSMEM 226 246
 CC FT DOMAIN 247 287
 CC FT DISULFID 29 117
 CC FT DISULFID 68 167
 CC FT CARBOHYD 100 100
 CC FT CAROXYD 149 149
 CC FT CAROXYD 200 200
 CC SQ SEQUENCE 287 AA; 32328 MW; 6AE8556ADC152578 CRC64;
 Query Match 50.3%; Score 703; DB 1; Length 287;
 Best Local Similarity 51.9%; Pred. No. 1.6e-47;
 Matches 149; Conservative 50; Mismatches 74; Indels 14; Gaps 6;
 QY 1 MKKQTWILTCIYQLLEFNPVKTGICRNRYNNKVDKLVANIPKRYMTITLKYVG 60
 Db 1 MKKQTWILTCIYQLLEFNPVKTGICRNRYNNKVDKLVANIPKRYMTITLKYVG 60
 QY 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSI--SEGISNYSIIDKLIVNIVDLVECKE 117
 Db 61 MDVLPSCWISSEMYVQLSDLTLDLKFNSI--SEGISNYSIIDKLIVNIVDLVECKE 117
 QY 118 NSSKD-LKSKSEPPRLTPEEPFRIFNRSIDAFKPVVAASETSCVVSSTLSPEKDS 175
 Db 121 DKNKDFIKENGLHYEDDFIPENFRIFNRSIDAFKPVVAASETSCVVSSTLSPEKDS 180
 QY 176 RVSATKPFMLPVAASSLRND-----SSSSNRKAKNPDPGSSLHMAMALPALFSLIIG 229
 Db 181 RVAAYKTIISFPVVAASSLRNDISGNTSSNKKKALGFISSISQIGISTALTSLSLIG 240
 QY 230 FAFGALYKRRKP-SLPRAVENIQIN--EEDNETSMQEKEREQEV 273
 Db 241 FILGAIYKTKTHPKSRPESNETIOCHGQENETSMQEKEREHLQV 287
 RESULT 7
 PRP3_DICDI 7
 ID PRP3_DICDI STANDARD; PRT; 989 AA.
 AC P54637;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (Protein-tyrosine-
 DE phosphate phosphohydrolase 3).
 GN (PRP3 OR PRP3) AND (PRP2 OR PRP3).
 OS Dictyostelium discoideum (Slime mold).

Query Match 7.0%; Score 97.5; DB 1; Length 403;

Best Local Similarity 26.2%; Pred. No. 1.9;

Matches 42; Conservative 22; Mismatches 59; Indels 37; Gaps 7;

QY 112 VECKENSSDKLKKSEFSPRELFTEPEFRIRNRSIDAKDFVASE-TSDCVSVSTLS 170
 DB 268 VHWIKDGPPLP-----APSPVLLPEVGH-----ADEGTYSCVATHPSH 307
 QY 171 PEKDSRVSVTKPPMLPPEVASSSLRNDSSSNRKAKNPPGDSLHWAMALPAFL-ITG 229
 DB 308 GPQES-----PPV---STRVETGDEGAESGVSGSLGTLALGLIGLVVA 354
 QY 230 FARGALYWKRRQP--SLTRAVENIQINEDNETISMLOEKE 267
 DB 355 LTVGAILMRKQPRRERKAPESQDEEERALEINQSEAE 394

RESULT 9

SCA4_RICFE STANDARD; PRT; 981 AA.

AC 09A37;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
 DE (Protein PS 120) (Fragment).
 GN SCA4 OR D.
 OS Rickettsia felis (Rickettsia azadi).
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiase; Rickettsia.
 OX NCBI_TaxID=42862;

RA SEQUENCE FROM N.A.
 RA Sekeyova Z., Roux V., Raoult D.;
 RT "Phylogenetic analysis of Rickettsia spp. by comparing the sequence of
 RT gene D coding for an intracytoplasmic protein";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -----

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CC EMBL: AF196973; AAK31304.1; -

DR Antigen.

KW Antigen.

FT NON_TER

FT NON_TER

SO SEQUENCE

981 AA: 107514 MW; 7F18F421E2C262E1 CRC64;

Query Match 6.9%; Score 97; DB 1; Length 981;

Best Local Similarity 23.8%; Pred. No. 6.4;

Matches 61; Conservative 33; Mismatches 84; Indels 78; Gaps 14;

QY 19 FNPVKTGICRNRYTNVND-----VTKLVANLPKDYMITLKYPGM-DV 63
 DB 628 FNTAKTEAI--QNTTTLVLDSPKAIKGTLESITRVAVESPLNGDKADYKMGGEA 685
 QY 64 LPSS-----CWISPMVVOISLTDLLDK-----FSNISEGLSNYSI----- 100
 DB 686 IASHTMAPTEKISTIEVEGVASISTIDEDKRLMTKGLVEGYEKKANPEITSEKTKA 745
 QY 101 ----IDKLIVNIVD--LVECVKE-----NSSDKLK-SFKSPPRRLTFPEEPRIF 144
 DB 746 VSRGIDKSTALPEKQALKDANEAALDRQNLTLEGAKRNLGEPFR-----DQINKA 801
 QY 145 NRSIDAFDFV-----ASETSDCVSVSTLSPEKD-SNVSATK-----PFMLPP 187

DB 802 QDVADALKNVITPVDAHPEKREVSDEEE-VVKTSSILINDISKLAIEKVNFRAMSPD 860

QY 188 VAASSLRNDSSSNRK 203

DB 861 GNLKTLLEEKRAESTKK 876

RESULT 10

MYSC_HUMAN

ID MYSC_HUMAN

AC 09NOX4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Myosin Vc (Myosin 5C).

GN MYOS5C.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Rodriguez O.C., Cheney R.E.;

RT "Cloning and characterization of myosin Vc, a third member of the

RT myosin V family in vertebrates";

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

CC -I- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC -I- SIMILARITY: CONTAINS 6 IQ DOMAINS.

CC -I- SIMILARITY: CONTAINS 1 DILUTE DOMAIN.

CC -----

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CC EMBL: AF27390; AAF78783.1; -

DR InterPro: IPR002710; DIL.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR001609; myosin_head.

DR Pfam: PF01843; DIL; 1.

DR Pfam: PF00063; myosin_head; 1.

DR PRINTS: PR00193; MYOSINHEAVY.

DR ProDom: PD000355; myosin_head; 1.

DR ProDom: PD003376; DIL; 1.

DR SMART: SM00015; IQ; 5.

DR SMART: SM00242; MYSC; 1.

DR PROSITE: PS50096; IQ; 4.

KW Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;

KW Coiled coil; Polymorphism.

FT DOMAIN 1 755

FT MYOSIN HEAD-LIKE.

FT 756 779

FT DOMAIN 2 806

FT 807 829

FT DOMAIN 3 854

FT 855 884

FT DOMAIN 4 1351

FT 1574 1679

FT COILED COIL (POTENTIAL).

FT DILUTE.

FT P -> L.

FT L -> S.

FT /FTID=VAR_010647.

FT VARIANT 634 634

FT SEQUENCE 1742 AA; 202793 MW; 25DD3082A7EB5AAB CRC64;

Query Match 6.9%; Score 96.5; DB 1; Length 1742;

Best Local Similarity 21.4%; Pred. No. 15;

Matches 60; Conservative 47; Mismatches 102; Indels 71; Gaps 14;

QY 38 KDVTKLVANLPKDYM--TLTKYVPMGMDVLPKSHCHTSEKAVVVOISLSD--LLDKFSN-- 90

Db 1369 EDEAKLIQNLIDLRKGVVNMIPG--LPAH--ILEMCVRYADSLDANMLKSLMNST 1423
 QY 91 -----ISEGLSNYSIIDKLVNIYDIVECYKENSNDKDKSKSPPERL-----FTPE 138
 Db 1424 INCIKQVAVHEHLEDFEMLFSLNCHPLNCIKQYSGEPEFKHNSPQONKNCJLNFDS 1483
 QY 139 EFERIENR-SIDAEKDFVAVSETN--DCVYSTLSPKDSRVSVTKPEMLPVAASSLRN 195
 Db 1484 EYKQILSDVAIRIYHQFIIMEKNIQPIIVPGMLEYESLQGISGLK-----TGERK 1535
 QY 196 DSSSN-----RKANPPGDSLSLHMAAALPALFSLITIGFAFG 233
 Db 1536 RSSSIDFDGYMTSVLQOLSTFYTTMCONGDP-----ELVROAVKQFLFICAVTLN 1589
 QY 234 ALYKKRPSLTRAENIQIINEEDNEISMLQE--KEREFQ 271
 Db 1590 SLFLRKDMCGRKGMQ-IRCN-----ISYLEMLKDKNKQ 1623

RESULT 11
 FDHA_METUA STANDARD; PRT; 378 AA.
 ID 060314:
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Putative formate dehydrogenase alpha chain (EC 1.2.1.2).
 GN M70006.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
 Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
 Uutterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RT Science 273:1058-1073(1996).
 RL Science 273:1058-1073(1996).
 CC -1- CATALYTIC ACTIVITY: Formate + NAD(+) = CO(2) + NADH.
 CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN), ZINC, FAD, MAY BIND 4 FE-4S
 CC CLUSTER (BY SIMILARITY).
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
 CC OXIDOREDUCTASE FAMILY.
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 CC -----
 CC EMBL: U67459; AAB97987.1; -
 CC HSSP: P07658; IAA6.
 DR TIR: MU0006; -
 DR InterPro: IPR001467; Molybdopterin.
 DR Pfam: PF00384; Molybdopterin; 2.
 DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; 1.
 DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
 DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; FALSE NEG.
 KM Hypothetical protein: Oxidoreductase: Zinc; Flavo-protein; Molybdenum;
 KM FAD; NAD; Iron-sulfur; 4Fe-4S; Complete proteome.
 FT METAL 8 8 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

FT METAL 11 11 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 15 15 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 43 43 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 378 AA; 42050 MW; EC013060FE2609AA CRC64;

Query Match 6.4%; Score 90; DB 1; Length 378;

Best Local Similarity 21.3%; Pred. No. 6.7;
 Matches 66; Conservative 31; Mismatches 91; Indels 122; Gaps 16;

QY 12 IYIQLLEFNLVKTG-----ICRNVTNNKQVT-----K 42
 Db 53 IYHEKRLKPLIKKNGKLVKATEWDEALSFIAEKIKYNADITFIASGCKTNEQNALRK 112
 QY 43 LV-----ANLKR-----DYMILKTVPGM-----DVLPSCHWISWVQLSDS 80
 Db 113 LVDSLAKIIGHICNSPKVNAVEVSTTIDENAKNIIITIGDFSEALIGKVIRAKK 172
 QY 81 LTDL-----LDKF-----SNISEGLSNYS-----IIDKLVTIVDLVECKE 117
 Db 173 GSKYITFTEKEKILKLNADFEVAVDVLGVDSLVNPKNTIIINAVPN-VDEIKTAK 231
 QY 118 NSSKDL--KKSFKSPPERL-----FTPEEFRTNRS-----IDAFK--DF 154
 Db 232 NKAKVLPVAKHNTVGATLIGIPALNKDEYFELLKNSKFLYIMGENPALVDKDKVVEF 291
 QY 155 VV-----ASENSDCVYSTLSPKDSRVSVTKPEMLPVAASSLRNSSSN--RKAK 205
 Db 292 LVVQDITMTETRAEMADVLPSTCWAERD-----GTPIINTDKRIQIKAKV 336
 QY 206 NPPGDSLSLHW 215
 Db 337 NPPGDAMDMDW 346

RESULT 12
 NRFF_HAEIN STANDARD; PRT; 370 AA.
 ID NRFF_HAEIN
 AC P44942;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c-type biogenesis protein nrff precursor.
 DE NRFF OR H10934.
 GN Haemophilus influenzae.
 OS Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,
 Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 Uutterback T.R., Hanna M.C., Nguyen D.T., Sauder D.W., Brandon R.C.,
 Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RT Science 269:496-512(1995).
 RL Science 269:496-512(1995).
 CC -1- FUNCTION: MAY BE REQUIRED FOR THE BIOGENESIS OF C-TYPE
 CC CYTOCHROMES. POSSIBLE SUBUNIT OF A HEME LYASE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE CCMH/CYCL/CC12/NRFF FAMILY.
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DR EMBL: U37775; AAC22592.1; ALT_INIT.
DR TIGR: H10934;
DR InterPro: IPR001440; TPR.
DR Pfam: PF00515; TPR; 1.
KW Cytochrome c-type biogenesis; Periplasmic; Heme; Signal;
KW Complete proteome.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 370 CYTOCHROME C-TYPE BIOGENESIS PROTEIN
FT BINDING 47 47 HEME (COVALENT) (POTENTIAL).
FT BINDING 50 50 HEME (COVALENT) (POTENTIAL).
SO SEQUENCE 370 AA; 42161 MW; 4023B680D7FA980 CRC64;

Query Match 6.4%; Score 89.5; DB 1; Length 370;
Best Local Similarity 25.6%; Pred. No. 7.1;
Matches 57; Conservative 25; Mismatches 82; Indels 59; Gaps 12;

QY 68 CWISEMYVQSDSLTDL-LDKFENISEGLSNYSIIDKLVNIVDDLYECVKNSSKDLKRS 126
DB 50 CONQNLVESNSPIAYDLRLVYKAMVDEGKSNQOIIDKMTARQDFV-----NYKPP 100
QY 127 FK-----SPEPRLEFTEEEFRIFNRSIDAFKDFVASETSDCVSSTLSPEKDSRYS 178
DB 101 FKNMTALLMLLPVALLIILAAVLIFYENR-----KQF-----SEKVVQQL--ENDETIS 148
QY 179 VYKPFLLPYVAASLLANDSSSSKRAKKNPPGSSLLHMAALPALFSLITGAFGALYW- 237
DB 149 -----LPSTFGSSSPKQGEPS--KLSKGVNSKIYF-----VFETLLI--ALPATYTF 192
QY 238 -----KKRQPSLTRAVENTIOINE--DNEISMLOEKER 268
DB 193 SLDRFSRVOGGQSMIECHNQVEMNDKHNENVEIKLQNKLR 235

RESULT 13
Y218_RICPR STANDARD; PRT; 292 AA.
AC 005944;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative glycosyl transferase Rp128 (EC 2.-----).
GN RP218.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RA MEDLINE=97419517; PubMed=9274032;
RA Anderson J.O., Andersson S.G.E.,
RT "Genomic rearrangements during evolution of the obligate
intraacellular parasite Rickettsia prowazekii as inferred from an
analysis of 5205 bp nucleotide sequence.",
RL Microbiology 143:2783-2795(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RA MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RT Sichenitz-Ponten T., Alsmark U.C.M., Podowsky R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.",
RL Nature 396:133-140(1998).
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. WAAE/KDTPX
CC SUBFAMILY.

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DR EMBL: Y11780; CAI72466.1; -
DR InterPro: IPR001173; Glycosyltransf_2.
DR Pfam: PF00535; Glycosyltransf_2; 1.
KW Hypothetical protein; Transferase; Glycosyltransferase;
KW Complete proteome.
SO SEQUENCE 292 AA; 33902 MW; 45EF7570B05A270 CRC64;

Query Match 6.4%; Score 89; DB 1; Length 292;
Best Local Similarity 21.1%; Pred. No. 5.8;
Matches 68; Conservative 53; Mismatches 111; Indels 90; Gaps 16;

QY 1 MKKTQWLTGCIYQLLFNPLVTEGICRRVYNNKVDYK---LVANLPKDYMTLKY 57
DB 1 MKKISTFIIT-----KNESARIARAINVKNTIDEVIYVNDNESTDVTIAIK 47
QY 58 VPGMDVLPSCWISSEM-VVQLSDSLTDLKFNISEGLSNYSIIDKLVNIVDDLYECVK 116
DB 48 TLGAQVIYKP-WLGVGQKSPAESMC-----VNWVLNIDDELDELDELDELDELDEL 98
QY 117 ENSKSDLKSSPK-----SPEPRLEFTEEEFRIFNRSIDAFKDFVASETSDCVS 166
DB 99 TSHNDRLAYQILKILNMGDQKPRMFAPLNRKCTRLNKKFASFN-TINSTTHDSVFE 157
QY 167 STLSPEKDSRVSVT-KPEMLPVVA-----ASSLNDSSSSKRAKKNP 207
DB 158 N-----KD--VDFTGKIYLLNGIAIYHSGTISBOLVKNKAFYSSEAKDLVYKQKRLSNP 210
QY 208 PGDSSLHMAALPALF-----SLITGAFGALYKRPKPSLTRAVENTIOI 253
DB 211 RLATEMTWC--FLKAFPIRRYFVGFDGVDISITFAFARFLRLAKRLDLSL---KSONV 264
QY 254 NEEDNEI-----SMLOEKER 268
DB 265 ITSDNYINCYGMDRSLQOKKR 286

RESULT 14
SCA4_RICAK STANDARD; PRT; 998 AA.
ID SCA4_RICAK
AC 09AIX9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigenic heat-stable 120 kDa protein (P8120) (120 kDa antigen)
DE (Protein PS 120) (Fragment).
GN SCA4 OR D.
OS Rickettsia akari.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=786;
RN [1]
RP SEQUENCE FROM N.A.
RC Sekeyova Z., Roux V., Raoult D.;
RA "Phylogenetic analysis of Rickettsia spp. by comparing sequence of the
RT 'gene D' coding for an intracytoplasmic protein.",
RL Submittal (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC 1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -----
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 CC -----
 CC EMBL: AF213016; AAK30691.1; .
 CC Antigen.
 KW NON_TER 1 1
 FT NON_TER 998 998
 SQ SEQUENCE 998 AA; 109328 MW; FCEBA3AC62DE5BD5 CRC64;

Query Match 6.4%; Score 89; DB 1; Length 998;
 Best Local Similarity 22.5%; Pred. No. 27;
 Matches 58; Conservative 37; Mismatches 77; Indels 86; Gaps 13;

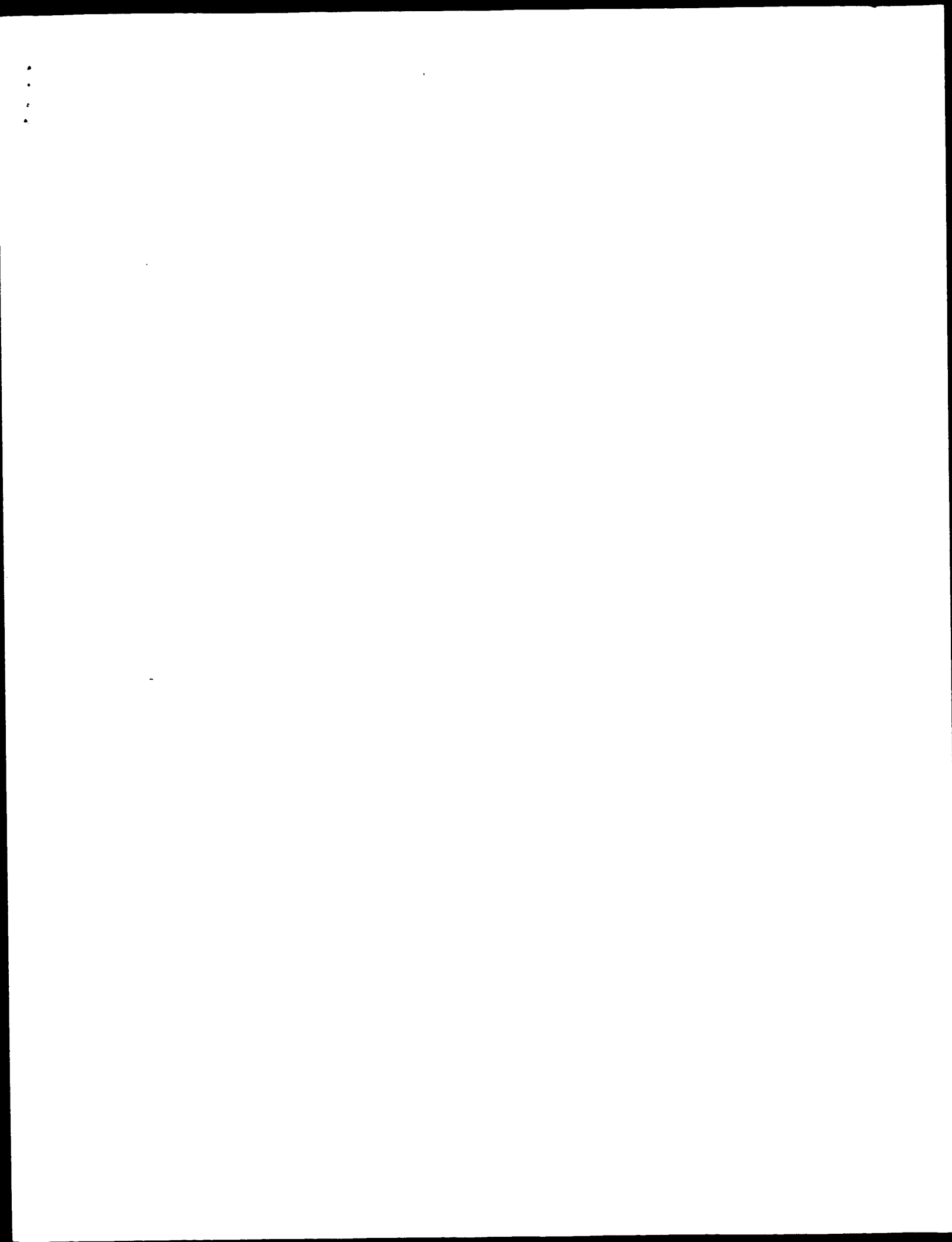
QY 19 FNLVTEGICRRVNNV-----VTKLVANLPKRYMTLKYVPGM-DV 63
 DB 636 FNTIAKTAAL--OKVTKVLDSPITAEIKGETLSTIKTIVAESPLNVQKTDIVKGMGA 693
 QY 64 LPSH-----CWISENVVQLSDSLFDLDDK-----FSN 90
 DB 694 IASHRTMAPTKTIAIESVETGVAKSTIDLEDKLMTKGLVDGIYBDKANPEITSEMKA 753
 QY 91 ISEGLSNVSTIDKLVNIVD-----LVECKENSSKDLK-KSPKSPPEPLFTPEEFRIE 144
 DB 754 VSKGVNSTAIPEDKQALKDASEALDRATQNTFELGKQNLDEPKPR-----DDIY 806
 QY 145 NRSID--AFKDFVAVSETSDCVSSSTLSPEKDSRVSVTKPFMLPPVAASLRNDSS-- 199
 DB 807 NKADIDVYALKN-----VTTVLDANPKEKREYSEEVW--NKTSSILNDISKIA 853
 QY 200 ---SNRKANPEGSSSL 213
 DB 854 IEKVNILRAMLSP-DSNL 870

RESULT 15
 YAE6_SCHPO STANDARD; PRT: 1325 AA.
 ID YAE6_SCHPO
 AC 009847;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Hypothetical 145.8 kDa protein C23D3.06C in chromosome I.
 GN SPAC23D3.06C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Niblett D., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL: Z64354; CAA91241.1; .
 KW Hypothetical protein.
 SQ SEQUENCE 1325 AA; 145776 MW; EEPD952FB7F0E6BD CRC64;

Query Match 6.3%; Score 88.5; DB 1; Length 1325;
 Best Local Similarity 20.7%; Pred. No. 43;
 Matches 60; Conservative 38; Mismatches 91; Indels 101; Gaps 12;

QY 18 LENDLVTEGICRRVNNV-----KDYTKLVANLPK-----DYMTLKYVPGMDV 63
 DB 717 IFGTAETQ-VEOKRPNNVLTKEFSFAPSDKSNFPAANIPSAGEGLDQKTSALP----- 771
 QY 64 LPSHCWISENVVQLSDSLFDLDDK-----SNISEG---LSNVSTIDK 104
 DB 772 -----STGITKLSNDNEKAESNETKGFNITIAKONKSSKSEKASVANMSALNKS 824
 QY 105 VNIIVDLVECKENSSKDLKSKSPPEPLFTPEEFRIINRSIDA-FKDFVAVSETSDC 163
 DB 825 TN-----NETSDSKPSLTKSP-----LEFSDADPTFEKRPSETPPF 861
 QY 164 VVSSTLSPEKDSRVSVT-----KPFMLPPVAASLRNDSSSNRKANPEGSSSLHWAAM 218
 DB 862 SPNKP-VEKESKQDVSTDSRSPFSFKAGCIDSKSPTEPEPTMAFSNISESEGWKLI 920
 QY 219 ALPALFSLILGFARFALYKRRQPSLTRAVENTIOINEDNEISMLOKER 268
 DB 921 EQPNVES-----EIEDODESSDLNGKRR 944

Search completed: August 18, 2002, 13:02:07
 Job time: 52 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:06:04 ; Search time 114.11 Seconds

(without alignments)
413.878 Million cell updates/sec

Title: US-09-604-325a-61

Perfect score: 1397

Sequence: 1 MKKTQWILTCIYLQLLFN.....NEEDNEISMLOEKEREPOEV 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMEL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_mhc:*
9: sp_mhc:*
10: sp_mhc:*
11: sp_mhc:*
12: sp_mhc:*
13: sp_mhc:*
14: sp_mhc:*
15: sp_mhc:*
16: sp_mhc:*
17: sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1218	87.2	245	4	Q9UOK7
2	1217.5	87.2	274	6	P79169
3	1187.5	85.0	274	6	Q95M19
4	1184.5	84.8	274	6	Q28132
5	1180.5	84.5	274	6	Q95N18
6	1158	82.9	273	11	Q9UOK7
7	1157	82.8	273	11	Q921N5
8	1156.5	82.8	267	6	P79368
9	1154.5	82.6	261	6	Q95MD2
10	1150	82.3	273	11	Q62524
11	1149	82.2	273	11	P97332
12	1117.5	80.0	256	6	O62765
13	1000	71.6	245	11	Q922E7
14	991.5	71.0	260	6	Q95MNS
15	978	70.0	245	11	O64222
16	865	61.9	208	11	Q64384

17	702	50.3	287	13	Q90314
18	589	42.2	253	13	Q90315
19	509	36.4	123	11	O61854
20	401.5	28.7	96	6	Q95MNS
21	375	26.8	271	13	Q9YGP2
22	251	18.0	54	4	Q16487
23	223.5	16.0	47	6	Q95MG7
24	214.5	15.4	51	6	Q9N1Y5
25	136	9.7	36	6	Q9TU74
26	106	7.6	465	16	Q97H56
27	105.5	7.6	1498	3	Q9P884
28	105.5	7.6	1498	3	Q96VK6
29	102	7.3	792	5	Q9BP03
30	100.5	7.2	1490	5	Q19545
31	100.5	7.2	402	11	Q35444
32	100.5	7.2	647	16	Q98P99
33	100	7.2	1501	3	Q96VL9
34	99	7.1	937	10	Q9MAL4
35	97.5	7.0	1107	3	Q12271
36	97	6.9	1447	16	Q9PQJ8
37	97	6.9	1566	11	Q9R1L5
38	96.5	6.9	475	11	Q9D6C8
39	96	6.9	3072	12	Q92645
40	95.5	6.8	484	5	O01626
41	95.5	6.8	614	5	Q9LQ29
42	95.5	6.8	683	2	Q50281
43	95.5	6.8	806	2	Q9L8P7
44	95.5	6.8	1515	3	Q96VK4
45	94.5	6.8	576	11	Q62970

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	245 AA.
Q9UOK7	Q9UOK7			
AC	Q9UOK7			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	STEM CELL FACTOR (STEM CELL FACTOR ISOFORM 2).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99160429; PubMed=10049787;			
RX	Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.;			
RT	"Parathyroid hormone-regulated production of stem cell factor in human			
RT	Biochem. Biophys. Res. Commun. 255:778-784(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Han C., Peng X., Yuan J., Qiang B.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AF119835; AAD22048.1; -			
DR	EMBL; AF400437; AAK92486.1; -			
DR	InterPro: IPR003452; SCF.			
DR	Pfam: PF02404; SCF; 1.			
SO	SEQUENCE 245 AA; 27903 MW; FF87983163A3C36 CRC64;			

Query Match 87.2%; Score 1218; DB 4; Length 245;
Best local Similarity 88.3%; Pred. No. 1.6e-94;
Matches 241; Conservative 1; Mismatches 3; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVETESICRNRYTNVKKDYTKLVANLPKRYMTTLKVVPS 60
Db 1 MKKTQWILTCIYLQLLFNPLVETESICRNRYTNVKKDYTKLVANLPKRYMTTLKVVPS 60
QY 61 MDVLPSCWISSEMYQLSDSLTDLDFKFSNIISGLSNYSIIDRLVNIIVDVLVECVKENS 120

```

Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVECEVENS 120
QY 121 KDKKSKSPERPLFPPEEFRIFNRSIDAFKDFVVAASESDCVSSTLSPEKDSRSVA 180
Db 121 KDKKSKSPERPLFPPEEFRIFNRSIDAFKDFVVAASESDCVSSTLSPEKGS 174
QY 181 KPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAALPALFSLIIGFAGALYMKR 240
Db 175 -----KAKNPPGDSLSHMAALPALFSLIIGFAGALYMKR 212
QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
Db 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245

RESULT 2
P79169 PRELIMINARY; PRT; 274 AA.
AC P79169;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE STEM CELL FACTOR.
GN SCF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97069946; PubMed=8912926;
RA Dunham S.P., Onions D.E.;
RT "The cloning and sequencing of cDNAs encoding two isoforms of feline
RT stem cell factor."
RL DNA Seq. 6:233-237(1996).
DR EMBL: D50833; BAO9445.1; -.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
SQ SEQUENCE 274 AA; 30987 MW; C5B78DB491237BE CRC64;

Query Match 87.2%; Score 1217.5; DB 6; Length 274;
Best Local Similarity 87.2%; Pred. No. 2e-94;
Matches 239; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKKTQWITLCIYLQDLLFNPLVKTGICRNVTNNVADYKLVANLPKDYMITLKYPG 60
Db 1 MKKTQWITLCIYLQDLLFNPLVKTGICRNVTNNVADYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVECEVENS 120
Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVECEVENS 120
QY 121 KDKKSKSPERPLFPPEEFRIFNRSIDAFKDFVVAASESDCVSSTLSPEKDSRSVA 179
Db 121 KDKKSKSPERPLFPPEEFRIFNRSIDAFKDFVVAASESDCVSSTLSPEKDSRSVA 180
QY 180 TRPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAALPALFSLIIGFAGALYMKR 239
Db 181 TRPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAALPALFSLIIGFAGALYMKR 240
QY 240 ROPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
Db 241 KOPNLTRIVENQIINEDNEISMLOEKEREFOEV 274

RESULT 3
P79169 PRELIMINARY; PRT; 274 AA.
AC P79169;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE STEM CELL FACTOR.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SHIBA; TISSUE=BRAIN;
RA Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;
RT "Identification of Splicing Isoforms of Caprine Stem Cell Factor
RT (SCF) Transcripts and Expression Patterns of the Two Major Isoforms,
RT gSCP825 and gSCP741, in the Brain and the Skin of Adult and Fetal
RT Shiba Goats (Capra hircus)."
RL Submitted (Mar-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB002152; BAB71733.1; -.
SQ SEQUENCE 274 AA; 31052 MW; BBFE69A509EF65D CRC64;

Query Match 85.0%; Score 1187.5; DB 6; Length 274;
Best Local Similarity 85.0%; Pred. No. 6.7e-92;
Matches 233; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKKTQWITLCIYLQDLLFNPLVKTGICRNVTNNVADYKLVANLPKDYMITLKYPG 60
Db 1 MKKTQWITLCIYLQDLLFNPLVKTGICRNVTNNVADYKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVECEVENS 120
Db 61 MDVLPSCWISSEWVQSLDSTLDLDFKNSISGLSNYSIIDKLVINVDLVECEVENS 120
QY 121 KDKKSKSPERPLFPPEEFRIFNRSIDAFKDFVVAASESDCVSSTLSPEKDSRSVA 179
Db 121 KDKKSKSPERPLFPPEEFRIFNRSIDAFKDFVVAASESDCVSSTLSPEKDSRSVA 180
QY 180 TRPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAALPALFSLIIGFAGALYMKR 239
Db 181 TRPFMLPVAASSLRNDSSSNRKAANPPGDSLSHMAALPALFSLIIGFAGALYMKR 240
QY 240 ROPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
Db 241 KOPNLTRIVENQIINEDNEISMLOEKEREFOEV 274

RESULT 4
Q28132 PRELIMINARY; PRT; 274 AA.
AC Q28132;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE STEM CELL FACTOR LONGER ISOFORM.
GN SCF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=SPLEEN;
RA Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.;
RT "Cloning and characterization of cDNAs encoding two normal isoforms of
RT bovine stem cell factor."
RL Biochim. Biophys. Acta 1223:148-150(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=BRAIN;
RA Kudo T.;
RT "Bovine counterpart of stem cell factor."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; D28934; BAA06061.1; -.
 DR EMBL; AB033716; BAA94808.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1
 SO SEQUENCE 274 AA; 31014 MW; D6C1DDB77B0CB12B CRC64;

Query Match 84.8%; Score 1184.5; DB 6; Length 274;
 Best Local Similarity 84.7%; Pred. No. 1.2e-91;
 Matches 232; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKVDYTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVIYVDLVECKENSS 120
 DB 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVIYVDLVECKENSS 120
 QY 121 KDLKSKFSPEPRLTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSPKDSRSVY 179
 DB 121 ENVAKSKSPPEPRQFTPEKFEIENRSIDAFKDF-VVASETSDCVVSTLSPKDSRSVY 180
 QY 180 TKPFMLPPVAASSLRNDSSSNRKAANPPGDSLSLHMAALPALFLSLIGFAFGALYWK 239
 DB 181 TKPFMLPPVAASSLRNDSSSNRKAANPPGDSLSLHMAALPALFLSLIGFAFGALYWK 240
 QY 240 RQPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 DB 241 KQPLTRTVENRQINEDNEISMLOEKEREFOEV 274

RESULT 5
 ID 095N18 PRELIMINARY; PRT; 274 AA.
 AC 095N18;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE STEM CELL FACTOR LONG ISOFORM.
 OS Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mustela.
 NCBI_TaxID=9667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bennett R.D., Murphy B.D.;
 RT Stem cell factor long form."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF013712; AAG37434.1; -.
 SO SEQUENCE 274 AA; 31034 MW; 5AC1619014AESE72 CRC64;

Query Match 84.5%; Score 1180.5; DB 6; Length 274;
 Best Local Similarity 84.3%; Pred. No. 2.6e-91;
 Matches 231; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKVDYTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVIYVDLVECKENSS 120
 DB 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVIYVDLVECKENSS 120
 QY 121 KDLKSKFSPEPRLTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSPKDSRSVY 179
 DB 121 ENVAKSKSPPEPRQFTPEKFEIENRSIDAFKDF-VVASETSDCVVSTLSPKDSRSVY 180
 QY 180 TKPFMLPPVAASSLRNDSSSNRKAANPPGDSLSLHMAALPALFLSLIGFAFGALYWK 239
 DB 181 TKPFMLPPVAASSLRNDSSSNRKAANPPGDSLSLHMAALPALFLSLIGFAFGALYWK 240

QY 240 RQPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 DB 241 KQPLTRTVENRQINEDNEISMLOEKEREFOEV 274

RESULT 6
 ID 090W24 PRELIMINARY; PRT; 273 AA.
 AC 090W24;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DE STEM CELL FACTOR KL-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Teramoto T., Nagashima M., Thorgerisson S.S.;
 RT "Rat-SCF-KL-1."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF071204; AAD02827.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1
 SO SEQUENCE 273 AA; 30712 MW; C0F56527DC93FD27 CRC64;

Query Match 82.9%; Score 1158; DB 11; Length 273;
 Best Local Similarity 82.4%; Pred. No. 2e-89;
 Matches 225; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKVDYTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWILTCIYLQLLFNPLVKTGICRNRYNNKVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVIYVDLVECKENSS 120
 DB 61 MDVPSHCWISSEWVQSLDLDLDFKFSNISBGLSNYSIIDKLVIYVDLVECKENSS 120
 QY 121 KDLKSKFSPEPRLTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSPKDSRSVY 180
 DB 121 KVKESLKKPETRNPFTPEEFRIENRSIDAFKDF-VVASETSDCVVSTLSPKDSRSVY 180
 QY 181 KPFMLPPVAASSLRNDSSSNRKAANPPGDSLSLHMAALPALFLSLIGFAFGALYWK 240
 DB 181 KPFMLPPVAASSLRNDSSSNRKAANPPGDSLSLHMAALPALFLSLIGFAFGALYWK 240
 QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273
 DB 241 QSSLTRAVENQINEDNEISMLOEKEREFOEV 273

RESULT 7
 ID 0921N5 PRELIMINARY; PRT; 273 AA.
 AC 0921N5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE SIMILAR TO KIT LIGAND.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011322; AAH11322.1; -.
 SO SEQUENCE 273 AA; 30661 MW; A7FC91E339320107 CRC64;

Query Match 82.8%; Score 1157; DB 11; Length 273;
 Best Local Similarity 82.8%; Pred. No. 2.4e-89;
 Matches 226; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKRTQWITTCIYQLLLFNPVLTGEGICRNRYNNVNDVTKLVANLPKDYMITLKYVG 60
 DB 1 MKRTQWITTCIYQLLLFNPVLTGEGICRNRYNNVNDVTKLVANLPKDYMITLKYVG 60

QY 61 MDVLPSCWISSEMYVQSLDSTLDLDFKFSNISGLSNYSIIDKLVINIVDDLVCEVKNSS 120
 DB 61 MDVLPSCWISSEMYVQSLDSTLDLDFKFSNISGLSNYSIIDKLVINIVDDLVCEVKNSS 120

QY 121 KDKKSPKSEPEPLTPEPEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDKKSPKSEPEPLTPEPEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180

QY 121 KDKKSPKSEPEPLTPEPEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 DB 121 KDKKSPKSEPEPLTPEPEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180

QY 181 KPFPMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYMKR 240
 DB 181 KPFPMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYMKR 240

QY 241 QPSLTRAVENTIOINEDNEISMLOEKEREFORV 273
 DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFORV 273

RESULT 8
 P79368 PRELIMINARY; PRT: 267 AA.

ID P79368; Q28591;
 AC 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE STEM CELL FACTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN (1)
 RP SEQUENCE OF 8-267 FROM N.A.
 RC TISSUE=OVARIAN FOLLICLE;
 RA TISSUE=OVARIAN FOLLICLE;
 RN Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 RP SEQUENCE OF 1-202 FROM N.A.
 RA McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haig D.;
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U89874; AAB49491.1; -;
 DR EMBL: Z50743; CAA90620.1; -;
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF. 1.
 FT NON_TER 267
 SEQUENCE 267 AA; 30148 MW; 9D9D959E4B9EC841 CRC64;

Query Match 82.8%; Score 1156.5; DB 6; Length 267;
 Best Local Similarity 85.0%; Pred. No. 2.6e-89;
 Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKRTQWITTCIYQLLLFNPVLTGEGICRNRYNNVNDVTKLVANLPKDYMITLKYVG 60
 DB 1 MKRTQWITTCIYQLLLFNPVLTGEGICRNRYNNVNDVTKLVANLPKDYMITLKYVG 60

QY 61 MDVLPSCWISSEMYVQSLDSTLDLDFKFSNISGLSNYSIIDKLVINIVDDLVCEVKNSS 120
 DB 61 MDVLPSCWISSEMYVQSLDSTLDLDFKFSNISGLSNYSIIDKLVINIVDDLVCEVKNSS 120

DB 61 MDVLPSCWISSEMYVQSLDSTLDLDFKFSNISGLSNYSIIDKLVINIVDDLVCEVKNSS 120
 QY 121 KDKKSPKSEPEPLTPEPEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 179
 DB 121 KDKKSPKSEPEPLTPEPEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180

QY 180 TKFPMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYMKR 239
 DB 181 TKFPMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYMKR 240

QY 240 RQPSLTRAVENTIOINEDNEISMLOEK 266
 DB 241 KQPSLTRAVENTIOINEDNEISMLOEK 267

RESULT 9
 Q95MD2 PRELIMINARY; PRT: 261 AA.

ID Q95MD2;
 AC Q95MD2;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MAST CELL GROWTH FACTOR (FRAGMENT).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9796;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Terry R.R., Mickelson J.R., Schmutz S., Cochran E.G., Bailey E.;
 RT "Equus caballus mast cell growth factor (MGF).";
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF401625; AAK94474.1; -;
 FT NON_TER 1
 FT NON_TER 1
 SEQUENCE 261 AA; 29526 MW; 16A3062105346E4B CRC64;

Query Match 82.6%; Score 1154.5; DB 6; Length 261;
 Best Local Similarity 86.6%; Pred. No. 3.7e-89;
 Matches 226; Conservative 19; Mismatches 15; Indels 1; Gaps 1;

QY 4 TQWITTCIYQLLLFNPVLTGEGICRNRYNNVNDVTKLVANLPKDYMITLKYVG 63
 DB 1 TQWITTCIYQLLLFNPVLTGEGICRNRYNNVNDVTKLVANLPKDYMITLKYVG 60

QY 64 LPSHCWISSEMYVQSLDSTLDLDFKFSNISGLSNYSIIDKLVINIVDDLVCEVKNSSKDL 123
 DB 61 LPSHCWISSEMYVQSLDSTLDLDFKFSNISGLSNYSIIDKLVINIVDDLVCEVKNSSKDL 120

QY 124 KSKSPSEPEPLTPEPEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 182
 DB 121 KSKSPSEPEPLTPEPEFRIFNRSIDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180

QY 183 FMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYMKR 242
 DB 181 FMLPPVAASSLRNDSSSNRKAAPPDSSSLHMAAMALPALFSLITGFAGALYMKR 240

QY 243 SLTRAVENTIOINEDNEISMLOEK 263
 DB 241 SLTRAVENTIOINEDNEISMLOEK 261

RESULT 10
 Q62524 PRELIMINARY; PRT: 273 AA.

ID Q62524;
 AC Q62524;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE MAST CELL GROWTH FACTOR.
 GN KITL OR MGF.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN NCB1_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/EL; TISSUE=BRAIN;
 RX MEDLINE=97032534; PubMed=8875893;
 RA Graw J., Loester J., Neuhauser-Klaus A., Pretsch N., Schmitt-John T.;
 RT "Molecular analysis of two new Steel mutations in mice shows a
 transversion or an insertion."
 RL Mamm. Genome 7:843-846(1996).
 DR EMBL: X99322; CA67698.1; -;
 DR MGD: MGI:96974; KIL.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF.
 FT VARIANT 193 193 P -> L.
 FT VARIANT 207 207 S -> A.
 SQ SEQUENCE 273 AA; 30645 MW; B3E9D0B72C734107 CRC64;

Query Match 82.3%; Score 1150; DB 11; Length 273;
 Best Local Similarity 82.4%; Pred. No. 9.4e-89;
 Matches 225; Conservative 19; Mismatches 29; Indels 0; Gaps 0;

QY 1 MKKTQWLTCTIYQLLFPNFKTEGICRRNRYNNKDVTKLVANLPKDYMTLKYVG 60
 DB 1 MKKTQWLTCTIYQLLFPNFKTEGICRRNRYNNKDVTKLVANLPKDYMTLKYVG 60
 QY 61 MDVLPSCMISWVYVSDSLTDLDFKFSNISGLSYSTIDKLVNIVDDLYCEKENS 120
 DB 61 MDVLPSCMISWVYVSDSLTDLDFKFSNISGLSYSTIDKLVNIVDDLYCEKENS 120
 QY 121 KDLKSKSPPEPLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVST 180
 DB 121 KDLKSKSPPEPLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVST 180
 QY 121 KDLKSKSPPEPLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVST 180
 DB 121 KDLKSKSPPEPLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVST 180
 QY 181 KPEMLPVAASLRNDSSSNRKAAPGDSILHMAALPALFSLITGAFGALYWKRR 240
 DB 181 KPEMLPVAASLRNDSSSNRKAAPGDSILHMAALPALFSLITGAFGALYWKRR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLOEKERFQEV 273
 DB 241 QPSLTRAVENIQINEEDNEISMLOEKERFQEV 273

RESULT 11
 P97332 PRELIMINARY; PRT; 273 AA.
 AC P97332;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MAST CELL GROWTH FACTOR.
 GN KITL OR MGF S1-3NEU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN NCB1_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=102/ELXC3H/EL; FI;
 RX MEDLINE=98025115; PubMed=9360640;
 RA Graw J., Neuhauser-Klaus, Pretsch;
 RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
 gene defines a novel allele at the Steel locus with a weak
 phenotype."
 RL Mutat. Res.; Mutat. Res. Genomics 382:75-78(1997).
 DR EMBL: Y10287; CAA71329.1; -;
 DR MGD: MGI:96974; KIL.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF.
 FT VARIANT 193 193 P -> L.

FT VARIANT 207 207 S -> A.
 SQ SEQUENCE 273 AA; 30618 MW; BC36F17A2C6F90C3 CRC64;

Query Match 82.2%; Score 1149; DB 11; Length 273;
 Best Local Similarity 82.4%; Pred. No. 1.1e-88;
 Matches 225; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

QY 1 MKKTQWLTCTIYQLLFPNFKTEGICRRNRYNNKDVTKLVANLPKDYMTLKYVG 60
 DB 1 MKKTQWLTCTIYQLLFPNFKTEGICRRNRYNNKDVTKLVANLPKDYMTLKYVG 60
 QY 61 MDVLPSCMISWVYVSDSLTDLDFKFSNISGLSYSTIDKLVNIVDDLYCEKENS 120
 DB 61 MDVLPSCMISWVYVSDSLTDLDFKFSNISGLSYSTIDKLVNIVDDLYCEKENS 120
 QY 121 KDLKSKSPPEPLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVST 180
 DB 121 KDLKSKSPPEPLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVST 180
 QY 121 KDLKSKSPPEPLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVST 180
 DB 121 KDLKSKSPPEPLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVST 180
 QY 181 KPEMLPVAASLRNDSSSNRKAAPGDSILHMAALPALFSLITGAFGALYWKRR 240
 DB 181 KPEMLPVAASLRNDSSSNRKAAPGDSILHMAALPALFSLITGAFGALYWKRR 240
 QY 241 QPSLTRAVENIQINEEDNEISMLOEKERFQEV 273
 DB 241 QPSLTRAVENIQINEEDNEISMLOEKERFQEV 273

RESULT 12
 062765 PRELIMINARY; PRT; 256 AA.
 AC 062765;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE STEM CELL FACTOR HOMOLOG (FRAGMENT).
 GN SCF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN NCB1_TaxID=9796;
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN.
 RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
 RT "An equine sequence homologous to stem cell factor (KIT-ligand)."
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF053498; AAC97076.1; -;
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF.
 FT NON_TER 1 256
 FT NON_TER 1 256
 SQ SEQUENCE 256 AA; 28933 MW; 9E4876CAEC7B55FF CRC64;

Query Match 80.0%; Score 1117.5; DB 6; Length 256;
 Best Local Similarity 86.3%; Pred. No. 4.6e-86;
 Matches 221; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 12 IYQLLFPNFKTEGICRRNRYNNKDVTKLVANLPKDYMTLKYVGMDVLPSCMIS 71
 DB 1 IYQLLFPNFKTEGICRRNRYNNKDVTKLVANLPKDYMTLKYVGMDVLPSCMIS 71
 QY 72 EMYVOLSLSLTLDFKFSNISGLSYSTIDKLVNIVDDLYCEKENSMDLKKFSKPE 131
 DB 72 EMYVOLSLSLTLDFKFSNISGLSYSTIDKLVNIVDDLYCEKENSMDLKKFSKPE 131
 QY 132 PRLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVSTKPPMLPVA 190
 DB 132 PRLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVSTKPPMLPVA 190
 QY 121 SRLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVSTKPPMLPVA 180
 DB 121 SRLTPEEFRIKNSIDAFKDFVAVSETSDCVSVSTLSPKDSRVSTKPPMLPVA 180
 QY 191 SSLRNDSSSNRKAAPGDSILHMAALPALFSLITGAFGALYWKRRQPSLTRAVEN 250

Db 181 SSTRDSSSSNRKASNTGTGDSNLQWMAALPAFSLVIGFAGALYKKRPMLTRAVEN 240
 QY 251 IQINEEDNEISMLOEK 266
 Db 241 IQINEEDNEISMLOEK 256

RESULT 13
 Q922E7
 ID 0922E7 PRELIMINARY; PRT; 245 AA.
 AC 0922E7;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE STEM CELL FACTOR KL-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Teramoto T., Nagashima M., Thorgeirsson S.S.;
 RT "Rat-SCF-KL-2."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF071205; AAD02828.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 DR SEQUENCE 245 AA; 27691 MW; 961511DAA6AE4F82 CRC64;

Query Match 71.6%; Score 1000; DB 11; Length 245;
 Best Local Similarity 72.2%; Pred. No. 3.2e-76;
 Matches 197; Conservative 18; Mismatches 30; Indels 28; Gaps 1;
 QY 1 MKKTQWIIITCIYQLLLFPNPLVTEGICRNRYTNVVDYTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWIIITCIYQLLLFPNPLVTEGICRNRYTNVVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEMYVOLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVOLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
 QY 121 KDLKSFSPERLPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 Db 121 KDLKSFSPERLPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 QY 121 KVVESLKKPRRTNPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 174
 Db 121 KVVESLKKPRRTNPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 174
 QY 181 KPFMLPVAASLNRDSSSSNRKAKNPBGDSSLHWAAMALPALFSLIIGFAGALYKKR 240
 Db 175 -----KAKPPEDPGLQNTAALPALISLVIGFAGALYKKR 212
 QY 241 OPSLTRAVENTIQINEEDNEISMLOEKREFFQEV 273
 Db 213 QSSLTRAVENTIQINEEDNEISMLOEKREFFQEV 245

RESULT 14
 Q95MNS
 ID 095MNS PRELIMINARY; PRT; 260 AA.
 AC 095MNS;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE STEM CELL FACTOR SHORT ISOFORM.
 OS Mus musculus (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mus.
 OC NCBI_TaxID=9667;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Bennett R.D., Murphy B.D.;
 RT "Stem cell factor in the mink uterus.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF323757; AAK73366.1; -.
 SQ SEQUENCE 260 AA; 29542 MW; A63111CEA8A50A34 CRC64;

Query Match 71.0%; Score 991.5; DB 6; Length 260;
 Best Local Similarity 72.1%; Pred. No. 1.8e-75;
 Matches 196; Conservative 22; Mismatches 25; Indels 29; Gaps 2;

QY 1 MKKTQWIIITCIYQLLLFPNPLVTEGICRNRYTNVVDYTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWIIITCIYQLLLFPNPLVTEGICRNRYTNVVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEMYVOLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVOLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
 QY 121 KDLKSFSPERLPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 179
 Db 121 KDLKSFSPERLPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 179
 QY 121 ENYKSPKNEPRHFAEDFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 175
 Db 121 ENYKSPKNEPRHFAEDFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 175
 QY 180 TKPFMLPVAASLNRDSSSSNRKAKNPBGDSSLHWAAMALPALFSLIIGFAGALYKKR 239
 Db 176 -----KAKPPEDPGLQNTAALPALISLVIGFAGALYKKR 212
 QY 240 OPSLTRAVENTIQINEEDNEISMLOEKREFFQEV 271
 Db 213 QSSLTRAVENTIQINEEDNEISMLOEKREFFQEV 244

RESULT 15
 Q64222
 ID 064222 PRELIMINARY; PRT; 245 AA.
 AC 064222;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE C-KIT LIGAND TRUNCATED TRANSMEMBRANE FORM KL-2.
 GN SL/STEEL.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10095;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA MEDLINE=92350001; PubMed=1378327;
 RA Hwang E.J., Nocka K.H., Buck J., Besmer P.;
 RT "Differential expression and processing of two cell associated forms
 of the kit-ligand: KL-1 and KL-2."
 RT Mol. Biol. Cell 3:349-362(1992).
 RL EMBL: S40534; AAB22555.2; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 DR transmembrane.
 KW SEQUENCE 245 AA; 27541 MW; 7816113BAFBE0E23B CRC64;

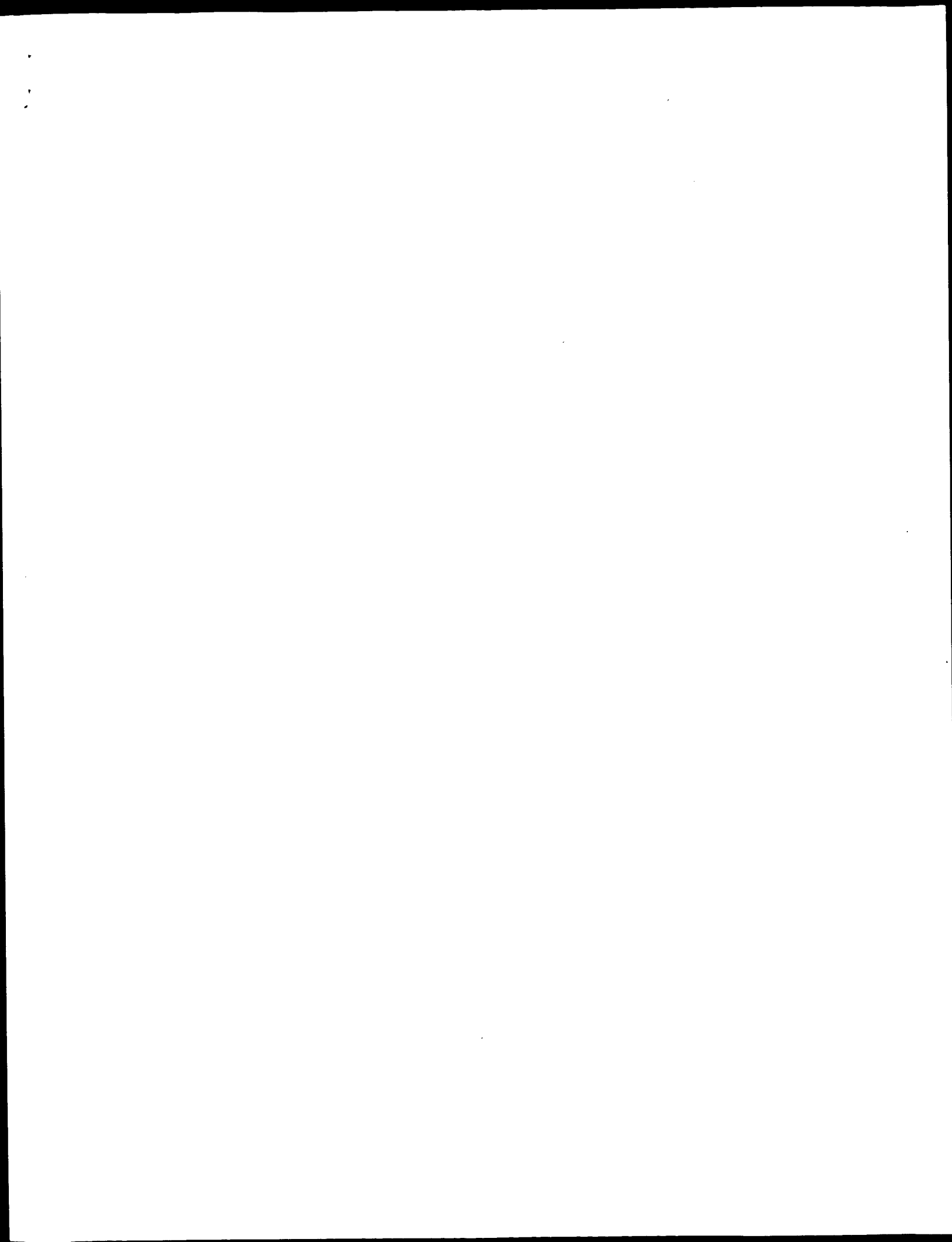
Query Match 70.0%; Score 978; DB 11; Length 245;
 Best Local Similarity 71.8%; Pred. No. 2.3e-74;
 Matches 196; Conservative 19; Mismatches 30; Indels 28; Gaps 1;

QY 1 MKKTQWIIITCIYQLLLFPNPLVTEGICRNRYTNVVDYTKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWIIITCIYQLLLFPNPLVTEGICRNRYTNVVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEMYVOLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVOLSDSLTDLDFKFSNISSEGLSNYSIIDKLVNIYDVLVECKENSS 120
 QY 121 KDLKSFSPERLPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 Db 121 KDLKSFSPERLPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 180
 QY 121 KVVESLKKPRRTNPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 174
 Db 121 KVVESLKKPRRTNPTPEEFRIENRSDAFKDFVAVSETSDCVVSTLSPKDSRVSVT 174

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QY 181 KPEMLPVAASSLRNDSSSNRKAKNPPGDSLHWAMALPALESLITGFAFGALYWKRR 240
Db 175 -----KAKAPEDSGLOLTAMALPALISLVIGFAFGALYWKRR 212
QY 241 QPSLTRAVENTIQINEEDNEISMLOEKEREFQEV 273
Db 213 QSSLTRAVENTIQINEEDNEISMLOEKEREFQEV 245
    
```

Search completed: August 18, 2002, 13:06:05
 Job time: 290 sec



PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH,
 XX WPI: 1991-119233/17.
 DR N-PSDB; AA011543.
 XX
 PR New naturally-occurring polypeptide stem cell factor analogues -
 PR have hematopoietic biological activity of stem cell factor and
 PR are used to treat eg leukopenia, AIDS, nerve damage and
 PR infertility
 XX
 PS Disclosure: Fig 44; 127pp; English.
 XX
 CC The SCF has the ability to stimulate growth of primitive
 CC progenitors including early hematopoietic progenitor cells and non-
 CC hematopoietic stem cells such as neural stem cells and primordial
 CC germ stem cells. The product may be used in a pharmaceutical
 CC compsn. for treating, in a mammal, leukopenia, thrombocytopenia,
 CC anaemia, AIDS, neoplasia, nerve damage, infertility and
 CC intestinal damage.
 CC See also AAR11708, AA011509-011543.
 CC
 XX
 SQ Sequence 245 AA:

Query Match 100.0%; Score 1262; DB 12; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.1e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYQLLEFNPVKTGICRNRYNNVKDVKLVANLPKDYMTLKYVPG 60
 DB 1 mktqtwtlctiyqlllfnpvktegicrntvnnvkdvklvanlpkdymltkyvp 60
 QY 61 MDVLPSCWISSEMYVOLDSLTDLDFKSNISSEGLSNYSIIDKLVNIYVDLVECKVENS 120
 DB 61 mdvlpshcwissemvqdsldtdldkfsniseqlsnysiidklyniyvdllveckvens 120
 QY 121 KDLKSKFSKSPRLFTPEEFRIENRSDAFKDFVVASETSDCVSSTLSPEKGRKKNP 180
 DB 121 kdlkskfsksprrlftpeeffriensidaefkdfvasetsdcvssstlspekgraknp 180
 QY 181 GDSSLHMAAALPALFSLITGFAGALYKKRQPSLTRAVENIOINEDNEISMLOEKER 240
 DB 181 gdsllhwaamaalpalfslitgfagalykkqpstraveniinqneedsismloqeker 240
 QY 241 EFOEV 245
 DB 241 efgev 245

RESULT 2

AAR83979
 ID AAR83979 standard; Protein; 245 AA.
 AC AAR83979;

15-MAY-1996 (first entry)

DE Human stem cell factor derived from 5637 bladder carcinoma cell line.
 XX
 XX
 XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
 KW thrombocytopenia; leukopenia; AIDS; immunodeficiency; bone graft;
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key
 FT Peptide
 FT /Label= sig_peptide
 FT 26..245
 FT Protein
 FT /Label= mat_SCF
 XX
 XX EP676470-AL.

PD 11-OCT-1995.
 XX
 PF 04-OCT-1990; 90EP-0105391.
 XX
 PR 01-OCT-1990; 90US-0589701.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90MO-US05548.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
 XX WPI: 1995-346090/45.
 DR N-PSDB; AA04891.
 XX
 PR New stem cell factor polypeptide(s) - for stimulating the growth of
 PR primitive progenitor cells, esp. for treating disorders involving
 PR blood cells
 XX
 PS Claim 9; Fig 44; 127pp; English.

CC AAR83979 is a human stem cell factor (SCF) derived from the 5637 bladder
 CC carcinoma cell line. Non-naturally occurring SCF and C-terminally
 CC truncated polypeptides, having amino acid sequences sufficiently
 CC duplicative of naturally occurring SCF, stimulate growth of primitive
 CC progenitors such as hematopoietic progenitor cells, neural stem
 CC cells and primordial germ stem cells. The peptides can be used in a
 CC composition for treating leukopenia, anaemia or thrombocytopenia,
 CC for enhancing engraftment of bone marrow during transplantation or
 CC for bone marrow recovery after chemotherapy or radiation-induced bone
 CC marrow aplasia or myelosuppression. They can also be used for
 CC treating neoplasia, nerve damage, infertility, intestinal damage or
 CC myeloproliferative disorders. Antibodies may be raised against the
 CC peptides for use in detection or neutralisation of SCF in serum. SCF
 CC may be useful for the treatment of AIDS and severe combined
 CC immunodeficiency (SCID) states alone or in combination with other
 CC factors such as IL-7.
 CC
 XX
 SQ Sequence 245 AA:

Query Match 100.0%; Score 1262; DB 16; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.1e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWITLCIYQLLEFNPVKTGICRNRYNNVKDVKLVANLPKDYMTLKYVPG 60
 DB 1 mktqtwtlctiyqlllfnpvktegicrntvnnvkdvklvanlpkdymltkyvp 60
 QY 61 MDVLPSCWISSEMYVOLDSLTDLDFKSNISSEGLSNYSIIDKLVNIYVDLVECKVENS 120
 DB 61 mdvlpshcwissemvqdsldtdldkfsniseqlsnysiidklyniyvdllveckvens 120
 QY 121 KDLKSKFSKSPRLFTPEEFRIENRSDAFKDFVVASETSDCVSSTLSPEKGRKKNP 180
 DB 121 kdlkskfsksprrlftpeeffriensidaefkdfvasetsdcvssstlspekgraknp 180
 QY 181 GDSSLHMAAALPALFSLITGFAGALYKKRQPSLTRAVENIOINEDNEISMLOEKER 240
 DB 181 gdsllhwaamaalpalfslitgfagalykkqpstraveniinqneedsismloqeker 240
 QY 241 EFOEV 245
 DB 241 efgev 245

RESULT 3

AAU05267
 ID AAU05267 standard; Protein; 245 AA.
 AC AAU05267;

XX 24-OCT-2001 (first entry)
 DT Human SCF protein isolated from the 5637 bladder carcinoma cell line.
 XX
 DE Human: stem cell factor; SCF; haematopoietic progenitor cell; AIDS;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; 5637 bladder carcinoma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..25 /Label= Signal_peptide
 FT Protein 26..245 /Label= Mature_SCF
 FT Protein /Label= Mature_SCF
 XX
 XX US6248319-B1.
 XX
 PD 19-JUN-2001.
 XX
 XX 24-MAY-1995; 95US-0449653.
 XX
 XX 10-APR-1991; 91US-0684535.
 XX 25-NOV-1992; 92US-0982285.
 XX 16-OCT-1989; 89US-0422383.
 XX 11-JUN-1990; 90US-0537198.
 XX 24-AUG-1990; 90US-0573616.
 XX 01-OCT-1990; 90US-0589701.
 XX 21-DEC-1993; 93US-0172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI: 2001-407312/43.
 DR N-PSDB; AAS10462.
 XX
 XX Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 XX Example 3; Fig 44; 210pp; English.
 PS
 XX The present sequence represents human stem cell factor (SCF). The cDNA
 CC encoding this sequence is isolated from the 5637 bladder carcinoma cell
 CC line. The sequence is described in an invention relating to novel stem
 CC cell factors, the polynucleotides encoding them and methods for
 CC producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral
 CC blood by administering a haematopoietically effective human stem cell
 CC factor polypeptide. The methods are useful for the treatment of blood
 CC disorders, including myelofibrosis, myelosclerosis, osteopetrosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folic acid deficiency.
 CC hypopigmentation disorders i.e. plebaldism and viral induced disorders,
 CC including AIDS.
 CC
 XX Sequence 245 AA:
 SQ
 Query Match 100.0%; Score 1262; DB 22; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1,1e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MKKTWTITCTCYDOLLFNPVKTETGICRRNRYNNKDVYKRYANLPKDYMITLKYVPG 60
 DB 1 mktgtwtitctcydollfnpvktetgicrrnrynnkvdxvcklvnlpkdymitlkyvpg 60

OY 61 MDVLSHCWISGMVYQVLSDTLTDLDFKFSNISEGISTNSIIDKLVNIYDVLVECYKENS 120
 DB 61 mdvlschcwisgmvyqlsdsltdldfkfsniseglsnysiddklnivddlvecykenns 120
 OY 121 KDLKSFKEPEPRILPTPEEFERFENRSDAFKDFVVASETSDCVVSTLSLEKGRKAKMP 180
 DB 121 kdlksfkspeprilptpeeferrfnrstdafkdfvvasetsdcvvsclspekgrakmp 180
 OY 181 GDSLSHMAAMALPALFSLITGFAPGALYWKRKPSLTRAVENTIOINEDNETSMLOEKER 240
 DB 181 gdslishmaamalpalfsllitgfalgalywkrkpstraveniqinednetsmlgeker 240
 OY 241 EQGEV 245
 DB 241 eqgev 245
 RESULT 4
 AAB98368
 ID AAB98368 standard; Protein; 245 AA.
 XX
 XX AAB98368;
 XX
 DT 21-AUG-2001 (first entry)
 XX
 DE Human SCF protein sequence SEQ ID NO:63.
 XX
 KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US6207454-B1.
 XX
 PD 27-MAR-2001.
 XX
 XX 31-DEC-1998; 98US-0224681.
 XX
 XX 21-DEC-1993; 93US-0172329.
 XX 24-MAY-1995; 95US-0449653.
 XX 12-JAN-1998; 98US-0005893.
 XX 25-NOV-1992; 92US-0982285.
 XX 16-OCT-1989; 89US-0422383.
 XX 11-JUN-1990; 90US-0537198.
 XX 24-AUG-1990; 90US-0573616.
 XX 01-OCT-1990; 90US-0589701.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI: 2001-366062/38.
 DR N-PSDB; AAH41345.
 XX
 XX Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing
 PT polynucleotide into cell in vitro -
 XX
 PS Claim 18; Fig 44; 210pp; English.
 XX
 XX The present invention describes a method for enhancing (E) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.

```

XX      Sequence      245 AA:
SQ
Query Match      100.0%; Score 1262; DB 22; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.1e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MKKTQWILTCIYQLLLFNPVKTEGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
DB      1 mktqtwtllctiyqlllfnplvktegicrnytnnvkvtklvanlpkdymltlkypg 60
OY      61 MDVLPSCWISSEWVQSDSLDLDKESNISSEISNYSTIIDKLVNVDLVCEKENS 120
DB      61 mdvlpshcwissemvqsdsltdldkfniseglsnysliidklnivddlvcevkens 120
OY      121 KDLKSEKSPPEPLTFPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKGAKNP 180
DB      121 kdlkksfksppepltfpeeffrlnrsidafkdfvasetsdcvssltlspekaknp 180
OY      181 GDSSLHWAMALPALFSLITGFAGALYKKRROPSTLRAVENIOINEEDNEISMLQEKER 240
DB      181 gds slhwaamalpal fslitgfagal ykk rpsltraveniqineedneism lqeker 240

OY      241 EFOEV 245
DB      241 efgev 245

RESULT 5
AAU02461
ID      AAU02461 standard; Protein; 245 AA.
AC      AAU02461:
XX      29-AUG-2001 (first entry)
DE      Human SCF protein isolated from the 5637 bladder carcinoma cell line.
XX      Human: stem cell factor; SCF: early haematopoietic progenitor cell;
KW      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW      anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
KW      5637 bladder carcinoma.
XX      Homo sapiens.
OS
XX      Key      location/Qualifiers
FH      Protein      1..25
FT      /label= Signal_peptide
FT      Protein      26..245
FT      /label= Mature_SCF

US6207417-B1.
27-MAR-2001.
XX      07-JUN-1995; 95US-0482918.
XX      21-DEC-1993; 93US-0172329.
XX      16-OCT-1989; 89US-0422383.
XX      11-JUN-1990; 90US-0537198.
XX      24-AUG-1990; 90US-0573616.
XX      01-OCT-1990; 90US-0589701.
XX      (ZSEB/) ZSEBO K M.
XX      (BOSS/) BOSSMAN R A.
XX      (SUGG/) SUGGS S V.
XX      (MART/) MARTIN F H.
XX      Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX      WPI: 2001-298941/31.
XX      N-PSDB: AAS04125.
DR

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```

XX      Novel nucleic acids encoding stem cell factor useful for treating
XX      disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
XX      disease, kala azar, anaemia and septicemia -
XX      Example 5; Fig 4A-44C; 209pp; English.
XX      The present sequence representing human SCF (stem cell factor)
XX      protein is isolated from the 5637 bladder carcinoma cell line. The
XX      present invention relates to novel stem cell factors
XX      (AAU02453-AAU02458, AAU02460) and the polynucleotides encoding them.
XX      SCF stimulate primitive progenitor cells including early haematopoietic
XX      progenitor cells. The invention also describes SCF peptides
XX      (AAU02462-AAU02481) and the oligonucleotides (AAS04081-AAS04117) used
XX      in the isolation of human and rat SCF sequences. The polynucleotide
XX      encoding SCF is useful for producing SCF and useful in gene therapy.
XX      It is useful for treating disorders involving blood cells such as
XX      myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
XX      Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive
XX      splenomegaly, kala azar, sarcoidosis, military tuberculosis, disseminated
XX      fungus disease, Fulminating septicemia, malaria, vitamin B12 and folate
XX      acid deficiency, pyridoxine deficiency, and hypopigmentation disorders
XX      such as piebaldism and vitiligo.
XX      Sequence      245 AA:
SQ
Query Match      100.0%; Score 1262; DB 22; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.1e-121;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MKKTQWILTCIYQLLLFNPVKTEGICRNRYNNKDVTKLVANLPKDYMITLKYPG 60
DB      1 mktqtwtllctiyqlllfnplvktegicrnytnnvkvtklvanlpkdymltlkypg 60
OY      61 MDVLPSCWISSEWVQSDSLDLDKESNISSEISNYSTIIDKLVNVDLVCEKENS 120
DB      61 mdvlpshcwissemvqsdsltdldkfniseglsnysliidklnivddlvcevkens 120
OY      121 KDLKSEKSPPEPLTFPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKGAKNP 180
DB      121 kdlkksfksppepltfpeeffrlnrsidafkdfvasetsdcvssltlspekaknp 180
OY      181 GDSSLHWAMALPALFSLITGFAGALYKKRROPSTLRAVENIOINEEDNEISMLQEKER 240
DB      181 gds slhwaamalpal fslitgfagal ykk rpsltraveniqineedneism lqeker 240

OY      241 EFOEV 245
DB      241 efgev 245

RESULT 6
AAU02767
ID      AAU02767 standard; Protein; 245 AA.
AC      AAU02767:
XX      29-AUG-2001 (first entry)
DE      Human SCF protein isolated from the 5637 bladder carcinoma cell line.
XX      Human: stem cell factor; SCF: early haematopoietic progenitor cell;
KW      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW      anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
KW      5637 bladder carcinoma.
XX      Homo sapiens.
OS
XX      Key      location/Qualifiers
FH      Protein      1..25
FT      /label= Signal_peptide
FT      Protein      26..245
FT

```

```

FT  /label= Mature_SCF
XX
XX  US6218148-B1.
XX
XX  17-APR-2001.
XX
XX  21-DEC-1993; 930S-0172329.
XX
XX  25-NOV-1992; 920S-0982255.
XX  16-OCT-1989; 890S-0422383.
XX  11-JUN-1990; 900S-0537198.
XX  24-AUG-1990; 900S-05373616.
XX  01-OCT-1990; 900S-0589701.
XX
XX  (AMGE-) AMGEN INC.
XX
XX  Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX  WPI: 2001-281051/29.
XX  N-PSDB; AAS04225.
XX
XX  Isolated DNA sequence, encoding polypeptide product useful for
XX  stimulating growth of early haematopoietic progenitor cells -
XX
XX  Example 5; Fig 44A-44C; 167pp; English.
XX
XX  The present sequence representing human SCF (stem cell factor)
XX  protein is isolated from the 5637 bladder carcinoma cell line. The
XX  present invention relates to novel stem cell factors
XX  (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
XX  encoding them. SCF stimulate primitive progenitor cells including early
XX  haematopoietic progenitor cells. The invention also describes SCF
XX  peptides (AAU02777-AAU02794) and the oligonucleotides
XX  (AAS04182-AAS04218) used in the isolation of human and rat SCF
XX  sequences. The polynucleotide encoding SCF is useful for producing
XX  SCF and useful in gene therapy. It is useful for treating disorders
XX  involving blood cells such as myelofibrosis, metastatic carcinoma,
XX  acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX  Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
XX  sarcoidosis, military tuberculosis, disseminated fungus disease,
XX  fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX  pyridoxine deficiency, and hypopigmentation disorders such as
XX  plebaldism and vitiligo.
XX
XX  Sequence 245 AA:
SO

```

Query Match 100.0%; Score 1262; DB 22; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.1e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKKTQWIIITCITLQLLRNPVLYKTGICRNRYTNVNVKDVTKLVANLPRDYMITEKYPG 60
DB 1 MKKTQWIIITCITLQLLRNPVLYKTGICRNRYTNVNVKDVTKLVANLPRDYMITEKYPG 60
QY 61 MDVLPSCWVISEWVQVSLDLDKFNISFGNSNYITDKIVYVDYIECKVENS 120
DB 61 MDVLPSCWVISEWVQVSLDLDKFNISFGNSNYITDKIVYVDYIECKVENS 120
QY 121 KDLKSKFKSPERPLTFPEEFPRIFNRSIDAFKDFVAVASETSCVVSSTLSPKGRAKNP 180
DB 121 KDLKSKFKSPERPLTFPEEFPRIFNRSIDAFKDFVAVASETSCVVSSTLSPKGRAKNP 180
QY 181 GDSSTLWAMALPALPSLTIGFAFGALWKKRQPSITRAVENIQINEEDNEISMLQEKER 240
DB 181 GDSSTLWAMALPALPSLTIGFAFGALWKKRQPSITRAVENIQINEEDNEISMLQEKER 240
QY 241 EFQEV 245
DB 241 EFQEV 245

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AAB73568
ID AAB73568 standard; Protein; 245 AA.
XX
XX  AAB73568;
XX
XX  07-AUG-2001 (first entry)
XX
XX  Human SCF protein isolated from the 5637 bladder carcinoma cell line.
XX
XX  Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX  blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX  anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX  5637 bladder carcinoma.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  Protein 1..25
XX  FT /label= Signal_peptide
XX  FT Protein 26..245
XX  FT /label= Mature_SCF
XX
XX  US6204363-B1.
XX
XX  20-MAR-2001.
XX
XX  25-NOV-1992; 920S-0982255.
XX
XX  10-APR-1991; 910S-0684535.
XX  16-OCT-1989; 890S-0422383.
XX  11-JUN-1990; 900S-0537198.
XX  24-AUG-1990; 900S-05373616.
XX  01-OCT-1990; 900S-0589701.
XX
XX  (AMGE-) AMGEN INC.
XX
XX  Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX  WPI: 2001-256683/26.
XX  N-PSDB; AAH23902.
XX
XX  New stem cell factor polypeptides and their analogs which stimulate
XX  growth of early hematopoietic progenitors, useful for treating aplastic
XX  anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX  disease
XX
XX  Claim 10; Fig 44A-44C; 166pp; English.
XX
XX  The present sequence representing human SCF (stem cell factor)
XX  protein is isolated from the 5637 bladder carcinoma cell line. The
XX  present invention relates to novel stem cell factors
XX  (AAB73561-AAB73568, AAB73571-AAB73576) and the polynucleotides
XX  encoding them. SCF stimulate primitive progenitor cells including early
XX  haematopoietic progenitor cells. The invention also describes SCF
XX  peptides (AAB73578-AAB73597) and the oligonucleotides
XX  (AAH23859-AAH23895) used in the isolation of human and rat SCF
XX  sequences. The polynucleotide encoding SCF is useful for producing
XX  SCF and useful in gene therapy. It is useful for treating disorders
XX  involving blood cells such as myelofibrosis, metastatic carcinoma,
XX  acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX  Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
XX  sarcoidosis, military tuberculosis, disseminated fungus disease,
XX  fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX  pyridoxine deficiency, and hypopigmentation disorders such as
XX  plebaldism and vitiligo.
XX
XX  Sequence 245 AA:
SO

```

Query Match 100.0%; Score 1262; DB 22; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.1e-121;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PT Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -

PS Claim 23; Fig 44; 123pp; English.

CC A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining
 CC haematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting the
 CC haematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC haematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a specifically claimed human SCF from the present invention.

XX Sequence 246 AA;

Query Match 99.2%; Score 1251.5; DB 21; Length 246;
 Best Local Similarity 99.6%; Pred. No. 1.3e-120;
 Matches 245; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKKTQ-TWILTCYIQLLLFNPVLTGEGICRRRVNNKVDYTKLVANLPKDYMITLKYVP 59
 DB 1 MKKTQ-TWILTCYIQLLLFNPVLTGEGICRRRVNNKVDYTKLVANLPKDYMITLKYVP 60
 QY 60 GMDVLPSCWISBMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDDLVCEVENS 119
 DB 61 GMDVLPSCWISBMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDDLVCEVENS 120
 QY 120 SKDLKSFSPERLFTPEEFRIINRSIDAFKDFVASETSDCVSSTLSPEKAKNP 179
 DB 121 SKDLKSFSPERLFTPEEFRIINRSIDAFKDFVASETSDCVSSTLSPEKAKNP 180
 QY 180 PGDSSLHMAAMALPALFSLIIGFAGALYWKKROPISLTRAVENTIOINEDENEISMLQEK 239
 DB 181 PGDSSLHMAAMALPALFSLIIGFAGALYWKKROPISLTRAVENTIOINEDENEISMLQEK 240
 QY 240 REFOEV 245
 DB 241 REFOEV 246

RESULT 10
 AAR11711

ID AAR11711 standard; Protein: 273 AA.

XX AAR11711;

XX 20-JUN-1991 (first entry)

XX Human Stem Cell Factor from HT1080 fibrosarcoma line.

XX Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..25
 XX FT /label= sig-peptide
 XX Protein 26..273

FT /label= mat-protein

XX EP423980-A.

XX 24-APR-1991.

XX 04-OCT-1990; 90EP-0310899.

XX 01-OCT-1990; 90US-0589701.

XX 16-OCT-1989; 89US-0422383.

XX 11-JUN-1990; 90US-0537198.

XX 24-AUG-1990; 90US-0573616.

XX 28-SEP-1990; 90MO-US05348.

XX (AMGE-) AMGEN INC.

XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;

XX WPI; 1991-119233/17.

XX N-PSDB; AAQ11542.

XX New naturally-occurring polypeptide stem cell factor analogues -

XX have haematopoietic biological activity of stem cell factor and

XX are used to treat eg leukopenia, AIDS, nerve damage and

XX infertility

XX Disclosure; Fig 42; 127pp; English.

XX Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 12; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQ-TWILTCYIQLLLFNPVLTGEGICRRRVNNKVDYTKLVANLPKDYMITLKYVP 60
 DB 1 MKKTQ-TWILTCYIQLLLFNPVLTGEGICRRRVNNKVDYTKLVANLPKDYMITLKYVP 60
 QY 61 MDVLPSCWISBMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDDLVCEVENS 120
 DB 61 MDVLPSCWISBMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDDLVCEVENS 120
 QY 121 MDVLPSCWISBMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDDLVCEVENS 174
 DB 121 MDVLPSCWISBMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVNIVDDLVCEVENS 180
 QY 175 -----KAKNPGDSSLHMAAMALPALFSLIIGFAGALYWKK 212
 DB 181 KPMPLPVAASLINDSSNRKAKPPGDSLHMAAMALPALFSLIIGFAGALYWKK 240
 QY 213 OPSLTRAVENTIOINEDENEISMLQEKREFOEV 245
 DB 241 QPSLTRAVENTIOINEDENEISMLQEKREFOEV 273

RESULT 11

ID AAR20647 standard; Protein: 273 AA.

XX AAR20647;

XX 30-APR-1992 (first entry)

DE		Human mast cell growth factor.
XX		
KW	hmGF-2.4:	hematopoietin; interleukin; IL-3; c-kit oncogene;
KW	proliferation.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	location/Qualifiers
FT	Peptide	1..25
FT		/label= signal
FT	Region	26..210
FT		/label= extracellular
FT	Region	/note= "claimed polypeptide"
FT		211..237
FT	Region	/label= transmembrane
FT		238..273
FT	Region	/label= intracellular
XX		
PN	WO9200376-A.	
PD	09-JAN-1992.	
XX		
PF	14-JUN-1991;	91WO-US04274.
XX		
PR	25-JUN-1990;	90US-0543264.
PR	10-AUG-1990;	90US-0565840.
PR	28-AUG-1990;	90US-0574152.
PR	21-SEP-1990;	90US-0586073.
PR	12-JUN-1991;	91US-0713715.
XX		
PA	(IMMU-) IMMUNEX CORP.	
XX		
PI	Williams DE, Lyman S;	
XX		
DR	WPI: 1992-041558/05. N-PsDB: AAQ20845.	
XX		
PT	New isolated DNA encoding human mast cell growth factor - useful in stimulating proliferation of haematopoietic cells with growth factor, to treat haemolytic and hypoproliferative anaemias	
XX		
PS	Claim 10; Fig 4; 59pp; English.	
XX		
CC	This human MGF has a mature extracellular region of 185 amino acids. There is a second form of hmGF (see AAQ20844) resulting from an alternative mRNA splicing event which deletes an exon encoding an additional 28 amino acids beginning at amino acid 148 of the mature protein. MGF is the ligand for the protein receptor expression product of the c-kit proto-oncogene. MGF can be used to augment the activity of other cytokines. It can influence early lymphoid or myeloid development. See also AAQ20842-3 and AAQ22204-7.	
CC		
XX		
SQ	Sequence 273 AA:	
	Query Match	97.5%; Score 1231; DB 13; Length 273;
	Best Local Similarity	89.4%; Pred.No.2e+118; 1; Indels 28; Gaps
	Matches 244; Conservative	0; Mismatches
OY	1 MKKTGTWIILCIQLDLLENPLVKEGICRNRVTNNVKDVKTLVANI.PKDYMITTLKYPG 60	1
DG	1 mktgtwiltclqlldllnplvktegicrnrvtnnvkdvtklvanlpkdymittlkypg 60	
OY	61 MDVLPSCHWISERNVOLSDSLTDLDKFSNISRGSLSNYSITDKLVNIYVDIVPCVRENLS 120	
DG	61 mdvlpschwisernvolstdsltdldkfnsisrgslsnysitdklvniyvdivpcvrenls 120	
OY	121 KDLIKSKSEPRFLPPEEFRIENSDIFKDFVVASETSDCVASTLSPEKG----- 174	
DG	121 kdlikskseprflppeefrifnsidafkdfvaasetscdvastlspekdsrsvst 180	
OY	175 -----KAKNPGGDSLHMAAMALPALFSLIGFAFGALYWKRR 212	

Db 181 kpm1pvaasslindssssnrkakpbgds1hwama1pal1s1l1gf1afg1aywkr 240

QY 213 QPSLRAVENIQINEDNEIEMLOEKREQEV 245
|||||
Db 241 qpsltraveniqineedneism1qekere1gev 273

RESULT 12

AAR83978
ID AAR83978 standard; Protein; 273 AA.

AC AAR83978;

XX Human stem cell factor derived from HT1080 fibrosarcoma cell line.
DE

AA stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
 KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft,
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.

05 Homo sapiens.

FH	Key	Location/qualifiers
FT	Peptide	1..25
FT		/label= sig_peptide
FT	Protein	26..248
FT		/label= mat_SCF

AA New stem cell factor polypeptide(s) - for stimulating the growth of
PT primitive progenitor cells, esp. for treating disorders involving
PT blood cells

AAR39/8 is a human stem cell factor (SCF) derived from the HT1080 fibrosarcoma cell line. Non-naturally occurring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally occurring SCF, stimulate growth of primitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertility, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7.

SQ Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 16; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWITLITCYQLLLFNPVLTGTCRNRTNNKVDYKLVANLPKDYMITLKYPG 60
 D 1 mktqtwtlctiyqlllfnplvktgicrnrvtnnvkdvtklvannlpkdymitlkyypg 60
 QY 61 MDVLPSCWISPMVVOLOSDSLDLKFSNISEGINSYIIDKLVNVDVLYECYKENS 120
 D 61 mdvlpshcwisemvvoqdsdlldkfsniseqinsyisldklvnvdvdlvecykens 120
 QY 121 KDLKSKSPSPRLPTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKG----- 174
 D 121 kdlkksfkspesprlftpeeffrlnrsidafkdfvasetsdcvvsstlspekdsrsvt 180
 QY 175 -----KAKNPGDSSLHMAALPALFSLITIGFAFGALYWKRR 212
 D 181 kpfmlpvaaslrndssssnrkaknpgdsslhmaamalpalfslligfagalywkrr 240
 QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 245
 D 241 qpsltravenlqineedneismqekerefev 273

RESULT 13

AAW27607
 ID AAW27607 standard; Protein; 273 AA.

AC AAW27607;

DT 28-APR-1998 (first entry)

DE Human recombinant stem cell factor protein.

KW Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor;
 KW SF; SLF; analogue; treatment; haematopoietic factor; progenitor cell;
 KW pigmentation disorder; haematopoietic disorder.

OS Homo sapiens.

EH Key Location/Qualifiers
 FT Peptide 1..25
 FT Protein /label= leader sequence 26..274

FT /note= "mature full length stem cell factor protein"

XX WO9738101-A1.

PD 16-OCT-1997.

PF 03-APR-1997; 97WO-US05541.

PR 05-APR-1996; 96US-0628428.

XX (AMGE-) AMGEN INC.

XX Lu HS;

DR WPI; 1997-512718/47.

XX Stem cell factor analogue N10D or N10D/N11D - useful to treat
 PT pigmentation disorder, AIDS, nerve damage, infertility, intestinal
 PT damage or haematopoietic disorder

PS Claim 2; Fig 1; 42pp; English.

XX This sequence represents a membrane bound form of a human recombinant
 CC stem cell factor (SCF). Stem cell factors are also known as mast cell
 CC growth factors (MCGF) or Steel factors (SF or SLF) are haematopoietic
 CC factors which act on haematopoietic progenitor cells. Analogues of a
 CC wild type SCF sequence have been constructed (see AAW27605 and AAW27606)

CC which have increased biological activity and stability compared to
 CC unmodified SCF and can be used to treat pigmentation disorders, e.g.
 CC vitilago, acquired immunodeficiency syndrome, nerve damage, infertility,
 CC intestinal damage or a haematopoietic disorder, e.g. leucopenia,
 CC thrombocytopenia or anaemia, enhance bone marrow engraftment during
 CC transplantation or bone marrow recovery following radiation, chemical or
 CC chemotherapeutic, induced bone marrow aplasia or myelosuppression,
 CC sensitize cells to chemotherapy or mobilise peripheral blood progenitor
 CC cells. It can also be used in an in vitro haematopoietic cell, preferably
 CC bone marrow or peripheral blood progenitor cell, culture medium, where
 CC the cells are optionally subsequently transfected with exogenous DNA.

SO Sequence 273 AA.

Query Match 97.5%; Score 1231; DB 18; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWITLITCYQLLLFNPVLTGTCRNRTNNKVDYKLVANLPKDYMITLKYPG 60
 D 1 mktqtwtlctiyqlllfnplvktgicrnrvtnnvkdvtklvannlpkdymitlkyypg 60
 QY 61 MDVLPSCWISPMVVOLOSDSLDLKFSNISEGINSYIIDKLVNVDVLYECYKENS 120
 D 61 mdvlpshcwisemvvoqdsdlldkfsniseqinsyisldklvnvdvdlvecykens 120
 QY 121 KDLKSKSPSPRLPTPEEFRIFNRSIDAFKDFVASETSDCVVSTLSPEKG----- 174
 D 121 kdlkksfkspesprlftpeeffrlnrsidafkdfvasetsdcvvsstlspekdsrsvt 180
 QY 175 -----KAKNPGDSSLHMAALPALFSLITIGFAFGALYWKRR 212
 D 181 kpfmlpvaaslrndssssnrkaknpgdsslhmaamalpalfslligfagalywkrr 240
 QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 245
 D 241 qpsltravenlqineedneismqekerefev 273

RESULT 14

AAV53284
 ID AAV53284 standard; Protein; 273 AA.

AC AAV53284;

DT 27-JUL-2000 (first entry)

DE Human SCF protein isolated from the HRI080 fibrosarcoma cell line.

KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
 KW primitive progenitor cell; haematopoietic disorder; syngeneic;
 KW allogeneic; autologous bone marrow transplant; gene therapy;
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
 KW cancer.

XX Homo sapiens.

OS Homo sapiens.

PN EP992579-A1.

XX EP992579-A1.

PD 12-APR-2000.

PF 04-OCT-1990; 99EP-0122861.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90MO-US05548.

PR 01-OCT-1990; 90US-0589701.

PR 04-OCT-1990; 90EP-0310899.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
 XX
 DR WPI: 2000-259135/23.
 N-PSDB: AAL13714.
 XX
 PT Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -
 XX
 PS Claim 22; Fig 42; 123pp; English.

XX A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining the
 CC haematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting the
 CC haematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC haematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a specifically claimed human SCF from the present invention.
 XX

SQ Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 21; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILFCIYQLLEFNPLVKTGICRNRYTNVNVKDYTKLVANPKDYMTLKYVPG 60
 DB 1 mktqtwtlctiyqlllfnplvktegicrnrvtvnvkvtklvaniplkdymltklyvpg 60
 QY 61 MDVLPSCWISSEWVOLSLSLTDLDKFSNISEGLSNYSIIIDKLVNIYVDLVECVKENS 120
 DB 61 mdvlpshcwissemvqjdsldldkfniseglsnyslidlkvniyvdllvecvkens 120
 QY 121 KDLKSKSPPEPLFTPEEFRIIRNSIDAFKDFVASETSDCVYSTLSPEKG----- 174
 DB 121 kdlkksfksppeplftpeeffrlnrsidafkdfvasetsdcvysstlspekdstsvst 180
 QY 175 -----KAKNPQCSLHWAMALPALFSLITGFAGALYKKR 212
 DB 181 kpfmlpvaasslndsssnrkkpvgdssllwamaalpalfslltfgafgalykkrr 240
 QY 213 QPSLRAVENIQINEDNEISMLOEKEREFOEV 245
 DB 241 qpsltraveniqineedneismloekerefev 273

RESULT 15

AAD05266
 ID AAD05266 standard; Protein: 273 AA.

XX AAD05266;

XX 24-OCT-2001 (first entry)

DE Human SCF protein isolated from the HT1080 fibrosarcoma cell line.

XX Human: stem cell factor; SCF: haematopoietic progenitor cell; AIDS;
 KW blood disorder; Hodgkin's disease; vitamin B12; folate acid deficiency;
 KW hypopigmentation disorder; viral disorder; HT1080 fibrosarcoma.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Protein 1..25
 FT /label= Signal_peptide
 FT 26..273
 FT /label= Mature_SCF
 FT Misc-difference 97
 FT /note= "Encoded by AAT"
 FT Misc-difference 258
 FT /note= "Encoded by AAT"
 FT US6248319-B1.

XX 19-JUN-2001.
 XX 24-MAY-1995; 95US-0449653.
 XX 10-APR-1991; 91US-0684535.
 XX 25-NOV-1992; 92US-0982255.
 XX 16-OCT-1989; 89US-0422383.
 XX 11-JUN-1990; 90US-0537198.
 XX 24-AUG-1990; 90US-0573616.
 XX 01-OCT-1990; 90US-0589701.
 XX 21-DEC-1993; 93US-0172329.

XX (ZSEB/) ZSEBO K M.
 XX (BOSS/) BOSSSELMAN R A.
 XX (SUGG/) SUGGS S V.
 XX (MART/) MARTIN F H.

XX Zsebo KM, Bosselmann RA, Suggs SV, Martin FH;

DR WPI: 2001-407312/43.
 N-PSDB: AAS10461.

PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX

PS Example 3; Fig 42; 210pp; English.

XX The present sequence represents human stem cell factor (SCF). The cDNA
 CC encoding this sequence is isolated from the HT1080 fibrosarcoma cell
 CC line. The sequence is described in an invention relating to novel stem
 CC cell factors, the polynucleotides encoding them and methods for
 CC producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral
 CC blood by administering a haematopoietically effective human stem cell
 CC factor polypeptide. The methods are useful for the treatment of blood
 CC disorders, including myelofibrosis, myelocytosis, osteopetrosis,
 CC metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's
 CC disease, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory
 CC anaemia, malaria, vitamin B12 and folate acid deficiency,
 CC hypopigmentation disorders i.e. piebaldism and viral induced disorders,
 CC including AIDS.
 XX

SQ Sequence 273 AA;

Query Match 97.5%; Score 1231; DB 22; Length 273;
 Best Local Similarity 89.4%; Pred. No. 2e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILFCIYQLLEFNPLVKTGICRNRYTNVNVKDYTKLVANPKDYMTLKYVPG 60
 DB 1 mktqtwtlctiyqlllfnplvktegicrnrvtvnvkvtklvaniplkdymltklyvpg 60
 QY 61 MDVLPSCWISSEWVOLSLSLTDLDKFSNISEGLSNYSIIIDKLVNIYVDLVECVKENS 120
 DB 61 mdvlpshcwissemvqjdsldldkfniseglsnyslidlkvniyvdllvecvkens 120


```

QY 121 KDLKSFKSPPEPRLFTPEEFRIENRSDAEKDFVVASSETSDCVVSTLSPKQ----- 174
Db 121 kdlkksfksppeprlftpeefritnrslakdivasetdsvsstlspkdsrsvt 180
QY 175 -----KAKNPPGDSLHWAAMALPALFSLIIGFAFGALYWK 212
Db 181 kpfmlpvaasslrndsssnrkaknppgdslnwaamalpalftslllgfagalywkr 240
QY 213 OPLTRAVENTIOINEDNEISMLOEKEREPOEV 245
Db 241 qpslctravenlqineedneismloekerefev 273

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Search completed: August 18, 2002, 13:08:02
 Job time: 407 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 13:04:01 ; Search time 41.62 Seconds
(without alignments)
143.784 Million cell updates/sec

Title: US-09-604-325A-63

Perfect score: 1262

Sequence: 1 MKRTQWILTCIYLQLLFN.....NEEDNEISMLQEKEREQEV 245

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCPUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	ID	Description
1	1262	100.0	245	4	US-08-482-918-63
2	1262	100.0	245	4	US-09-224-681-63
3	1262	100.0	245	4	US-08-336-728A-63
4	1231	97.5	273	1	US-08-220-379B-2
5	1231	97.5	273	2	US-08-628-428-9
6	1231	97.5	273	4	US-08-482-918-49
7	1231	97.5	273	4	US-08-482-918-61
8	1231	97.5	273	4	US-09-224-681-49
9	1231	97.5	273	4	US-09-224-681-61
10	1231	97.5	273	4	US-08-336-728A-48
11	1231	97.5	273	4	US-08-336-728A-49
12	1231	97.5	273	4	US-08-336-728A-61
13	1231	97.5	273	4	US-08-482-918-48
14	1231	97.5	273	4	US-08-482-918-50
15	1231	97.5	273	4	US-08-482-918-52
16	1231	97.5	273	4	US-08-482-918-54
17	1231	97.5	273	4	US-08-482-918-56
18	1231	97.5	273	4	US-08-482-918-58
19	1231	97.5	273	4	US-08-482-918-60
20	1231	97.5	273	4	US-08-482-918-62
21	1231	97.5	273	4	US-08-482-918-64
22	1231	97.5	273	4	US-08-482-918-66
23	1231	97.5	273	4	US-08-482-918-68
24	1231	97.5	273	4	US-08-482-918-70
25	1231	97.5	273	4	US-08-482-918-72
26	1231	97.5	273	4	US-08-482-918-74
27	1231	97.5	273	4	US-08-482-918-76

28	1012.5	80.2	274	4	US-08-336-728A-53	Sequence 53, Appl
29	1007	79.8	273	4	US-08-482-918-53	Sequence 53, Appl
30	1007	79.8	273	4	US-09-224-681-53	Sequence 53, Appl
31	992	78.6	273	4	US-08-482-918-42	Sequence 42, Appl
32	992	78.6	273	4	US-09-224-681-42	Sequence 42, Appl
33	992	78.6	273	4	US-08-336-728A-42	Sequence 42, Appl
34	992	78.6	273	4	US-08-336-728A-54	Sequence 54, Appl
35	991	78.5	273	1	US-08-220-379B-6	Sequence 6, Appl
36	991	78.5	273	4	US-08-482-918-55	Sequence 55, Appl
37	991	78.5	273	4	US-09-224-681-55	Sequence 55, Appl
38	991	78.5	273	4	US-08-336-728A-55	Sequence 55, Appl
39	985	78.1	273	4	US-08-482-918-54	Sequence 54, Appl
40	985	78.1	273	4	US-09-224-681-54	Sequence 54, Appl
41	978	77.5	273	1	US-08-341-456A-11	Sequence 11, Appl
42	978	77.5	273	2	US-08-478-414A-11	Sequence 11, Appl
43	978	77.5	273	3	US-08-325-240A-11	Sequence 11, Appl
44	978	77.5	273	4	US-08-898-982-11	Sequence 11, Appl
45	890	70.5	208	4	US-08-836-252A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-482-918-63
Sequence 63, Application US/08482918
Patent No. 6207417

GENERAL INFORMATION:

APPLICANT: Zsebo, Krisztina M.

APPLICANT: Bosseman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,918

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 01017/33005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEX: 312/474-0448

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 245 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-482-918-63

Query Match 100.0%; Score 1262; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKRTQWILTCIYLQLLFNPLVTEGICRNRRTNNKDYTKLVANIPKDYMTLKYVPG 60
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Db 1 MKKTQWILTCIYLQLLFNPVKTEGICRNRTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISEMNVQVSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDVLVECYKENS 120
Db 61 MDVLPSCWISEMNVQVSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDVLVECYKENS 120
QY 121 KDLKSKFSPEPRLEFTEPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNP 180
Db 121 KDLKSKFSPEPRLEFTEPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNP 180
QY 181 GDSLSLHMAAALPALFSLIIGFAGALYWKKROPSLTRAVENIQINEEDNEISMLOEKER 240
Db 181 GDSLSLHMAAALPALFSLIIGFAGALYWKKROPSLTRAVENIQINEEDNEISMLOEKER 240
QY 241 EFOEV 245
Db 241 EFOEV 245

RESULT 2
; Sequence 63, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TRANSFER WITH STEM CELL FACTOR (SCF) POLYPEPTIDE
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-224-681-63

Query Match 100.0%; Score 1262; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLQLLFNPVKTEGICRNRTNNVKDVKLVANLPKDYMITLKYVG 60
Db 1 MKKTQWILTCIYLQLLFNPVKTEGICRNRTNNVKDVKLVANLPKDYMITLKYVG 60
QY 61 MDVLPSCWISEMNVQVSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDVLVECYKENS 120
Db 61 MDVLPSCWISEMNVQVSDSLDLDKFSNISSEGLSNYSIIDKLVNIYDVLVECYKENS 120
QY 121 KDLKSKFSPEPRLEFTEPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNP 180
Db 121 KDLKSKFSPEPRLEFTEPEEFRIFNRSIDAFKDFVVASETSDCVSSSTLSPKGAKNP 180
QY 181 GDSLSLHMAAALPALFSLIIGFAGALYWKKROPSLTRAVENIQINEEDNEISMLOEKER 240
Db 181 GDSLSLHMAAALPALFSLIIGFAGALYWKKROPSLTRAVENIQINEEDNEISMLOEKER 240
QY 241 EFOEV 245
Db 241 EFOEV 245

RESULT 3
; Sequence 63, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-63

Query Match 100.0%; Score 1262; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYLLQLLFPNLYTEGICRNRYNNKDYTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWILTCIYLLQLLFPNLYTEGICRNRYNNKDYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCWISEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDVLECKENSS 120
DB 61 MDVLPSCWISEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDVLECKENSS 120
QY 121 KDLKSKSPERLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKAKNP 180
DB 121 KDLKSKSPERLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKAKNP 180
QY 181 GDSLSHMAAALPALPSLIGFAFGALYWKKROPSLTRAVENTIOINEDNEISMLQEKER 240
DB 181 GDSLSHMAAALPALPSLIGFAFGALYWKKROPSLTRAVENTIOINEDNEISMLQEKER 240
QY 241 EROEV 245
DB 241 EROEV 245

RESULT 4
US-08-220-379B-2
Sequence 2, Application US/08220379B
Patent No. 5525708
GENERAL INFORMATION:
APPLICANT: No. 5525708ka, Karl
APPLICANT: Lobell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B

FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytomed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: cleavage site
LOCATION: 164..165
US-08-220-379B-2

Query Match 97.5%; Score 1231; DB 1; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYLLQLLFPNLYTEGICRNRYNNKDYTKLVANLPKDYMTTLKYPG 60
DB 1 MKKTQWILTCIYLLQLLFPNLYTEGICRNRYNNKDYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCWISEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDVLECKENSS 120
DB 61 MDVLPSCWISEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVNIYDDVLECKENSS 120
QY 121 KDLKSKSPERLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKAKNP 180
DB 121 KDLKSKSPERLFTPEEFRIENRSDAFKDFVVASETSDCVVSTLSPEKAKNP 180
QY 175 -----KAKNP GDSLSHMAAALPALPSLIGFAFGALYWKK 212
DB 181 KFPMLPVAASSLRNDSSSNRKNKPNP GDSLSHMAAALPALPSLIGFAFGALYWKK 240
QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREPOEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLQEKEREPOEV 273

RESULT 5
US-08-628-428-9
Sequence 9, Application US/08628428
Patent No. 5885962
GENERAL INFORMATION:
APPLICANT: Lu, Hsieng
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846

REFERENCE/DOCKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..273
OTHER INFORMATION: /note= "NOTE: Mature full length
1-248 SCF protein begins at amino acid 26; amino acid 1-25
OTHER INFORMATION: include Met and leader sequences for membrane band form of hu
OTHER INFORMATION: recombinant SCF."
US-08-628-428-9

Query Match 97.5%; Score 1231; DB 2; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPLVTEGICRNKRVNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPLVTEGICRNKRVNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISWVYVOLSITDLDKFSNISEGLSNYSIIDKLVIYDDLVCEYKENS 120
DB 61 MDVLPSCWISWVYVOLSITDLDKFSNISEGLSNYSIIDKLVIYDDLVCEYKENS 120
QY 121 KDLKSKFSPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKG----- 174
DB 121 KDLKSKFSPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKSRVSVT 180
QY 175 -----KAKNPPGDSLSHMAAMALPALSILIGFAFGALYMKR 212
DB 175 -----KAKNPPGDSLSHMAAMALPALSILIGFAFGALYMKR 212
QY 213 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 245
DB 213 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273

RESULT 6
US-08-482-918-49
Sequence 49, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION NUMBER: 312/474-6300

REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-49

Query Match 97.5%; Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPLVTEGICRNKRVNNKDVTKLVANLPKDYMITLKYPG 60
DB 1 MKKTQWILTCIYQLLLFNPLVTEGICRNKRVNNKDVTKLVANLPKDYMITLKYPG 60
QY 61 MDVLPSCWISWVYVOLSITDLDKFSNISEGLSNYSIIDKLVIYDDLVCEYKENS 120
DB 61 MDVLPSCWISWVYVOLSITDLDKFSNISEGLSNYSIIDKLVIYDDLVCEYKENS 120
QY 121 KDLKSKFSPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKG----- 174
DB 121 KDLKSKFSPEPLFTPEEFRIENRSIDAFKDFVVASETSDCVVSTLSPEKSRVSVT 180
QY 175 -----KAKNPPGDSLSHMAAMALPALSILIGFAFGALYMKR 212
DB 175 -----KAKNPPGDSLSHMAAMALPALSILIGFAFGALYMKR 212
QY 213 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 245
DB 213 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENTIOINEEDNEISMLQEKEREFOEV 273

RESULT 7
US-08-482-918-61
Sequence 61, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION NUMBER: 01017/33005
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-482-918-61

Query Match 97.5%; Score 1231; DB 4; Length 273;
 Best Local Similarity 89.4%; Pred. No. 4e-122;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTOTWILTCIYIQLLFLNPLVTEGICRNRVTNNVADYTKLVANLPKDYMITLKYVG 60
 DB 1 MKKTOTWILTCIYIQLLFLNPLVTEGICRNRVTNNVADYTKLVANLPKDYMITLKYVG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVIYDDIVECVKENS 120
 DB 61 MDVLPSCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVIYDDIVECVKENS 120
 QY 121 KDILKSFSPERLFTPEEFRIFRNSIDAFKDFVASETSDCVVSTLSPKSG----- 174
 DB 121 KDILKSFSPERLFTPEEFRIFRNSIDAFKDFVASETSDCVVSTLSPKSGRVSVT 180
 QY 175 -----KAKNPPGSSSLHMAAMALPALFSLITGFAGALYWKRR 212
 DB 181 KPFLMPVAAASSLRNDSSSNRKKNPBGSSSLHMAAMALPALFSLITGFAGALYWKRR 240
 QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 245
 DB 241 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 273

RESULT 8

US-09-224-681-49
 Sequence 49, Application US/09224681
 Patent No. 6207454
 GENERAL INFORMATION:
 APPLICANT: Zsebo, Krisztina M.
 APPLICANT: Bosselman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/224,681
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/005,893
 FILING DATE: 12-JAN-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/449,653
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255
 FILING DATE: 25-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/569,701
 FILING DATE: 01-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/573,616
 FILING DATE: 24-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/537,198
 FILING DATE: 11-JUN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/422,383
 FILING DATE: 16-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W.
 REGISTRATION NUMBER: 36,107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX:
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-224-681-49

Query Match 97.5%; Score 1231; DB 4; Length 273;
 Best Local Similarity 89.4%; Pred. No. 4e-122;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTOTWILTCIYIQLLFLNPLVTEGICRNRVTNNVADYTKLVANLPKDYMITLKYVG 60
 DB 1 MKKTOTWILTCIYIQLLFLNPLVTEGICRNRVTNNVADYTKLVANLPKDYMITLKYVG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVIYDDIVECVKENS 120
 DB 61 MDVLPSCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVIYDDIVECVKENS 120
 QY 121 KDILKSFSPERLFTPEEFRIFRNSIDAFKDFVASETSDCVVSTLSPKSG----- 174
 DB 121 KDILKSFSPERLFTPEEFRIFRNSIDAFKDFVASETSDCVVSTLSPKSGRVSVT 180
 QY 175 -----KAKNPPGSSSLHMAAMALPALFSLITGFAGALYWKRR 212
 DB 181 KPFLMPVAAASSLRNDSSSNRKKNPBGSSSLHMAAMALPALFSLITGFAGALYWKRR 240
 QY 213 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 245
 DB 241 QPSLTRAVENTIOINEDNEISMLQEKEREFOEV 273

RESULT 9

US-09-224-681-61
 Sequence 61, Application US/09224681
 Patent No. 6207454
 GENERAL INFORMATION:
 APPLICANT: Zsebo, Krisztina M.
 APPLICANT: Bosselman, Robert A.
 APPLICANT: Suggs, Sidney V.
 APPLICANT: Martin, Francis H.
 TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-61

Query Match 97.5%; Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTGEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLLFNPVLTGEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCHWISEWVOLSITDLDKFSNISSEGLSNYSIIDKLVIYVDLVECKENSS 120
DB 61 MDVLPSCHWISEWVOLSITDLDKFSNISSEGLSNYSIIDKLVIYVDLVECKENSS 120
QY 121 KDKKSFSEPEPLTPEPEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKGS----- 174
DB 121 KDKKSFSEPEPLTPEPEFRIFNRSIDAFKDFVVASETSDCVVSTLSPKGSRSVST 180
QY 175 -----KAKNPQDSSLIHMAAALPALFSLITIGFAFGALYWKRR 212
DB 181 KPEMLPVAASLRNDSSSSNRKAKNPQDSSLIHMAAALPALFSLITIGFAFGALYWKRR 240
QY 213 QPSLTRAVENTIQINEDNEISMLOEKEREFQEV 245

DB 241 QPSLTRAVENTIQINEDNEISMLOEKEREFQEV 273

RESULT 10
US-08-336-728A-48
Sequence 48, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728A-48

Query Match 97.5%; Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPVLTGEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
DB 1 MKKTQWILTCIYQLLLFNPVLTGEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCHWISEWVOLSITDLDKFSNISSEGLSNYSIIDKLVIYVDLVECKENSS 120

Db 61 MDVLPSCWISSEMYVOLSDSLDLDKFSNISSEGLSNISIDKLVNIYDVLVECKENSS 120
Qy 121 KDLKSFSPBRLFTPEEFRIINRSIDAKDFVVASSETSDCVVSTLSPKSG----- 174
Db 121 KDLKSFSPBRLFTPEEFRIINRSIDAKDFVVASSETSDCVVSTLSPKSGSRVSVT 180
Qy 175 -----KAKNPQDSSLHMAAMALPALFSLITIGFAFGALYMKR 212
Db 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLITIGFAFGALYMKR 240
Qy 213 QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 245
Db 241 QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 273

RESULT 11
US-08-336-728A-49
; Sequence 49, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-728A-49

Query Match 97.5%; Score 1231; DB 4; Length 273;
Best local similarity 89.4%; Pred No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
Qy 1 MKTQWIIITCIYQLQLFLNPLVKTEGICRNVTNNKXDVTKLVANLPKDYMITLKYVG 60
Db 1 MKTQWIIITCIYQLQLFLNPLVKTEGICRNVTNNKXDVTKLVANLPKDYMITLKYVG 60
Qy 61 MDVLPSCWISSEMYVOLSDSLDLDKFSNISSEGLSNISIDKLVNIYDVLVECKENSS 120
Db 61 MDVLPSCWISSEMYVOLSDSLDLDKFSNISSEGLSNISIDKLVNIYDVLVECKENSS 120
Qy 121 KDLKSFSPBRLFTPEEFRIINRSIDAKDFVVASSETSDCVVSTLSPKSG----- 174
Db 121 KDLKSFSPBRLFTPEEFRIINRSIDAKDFVVASSETSDCVVSTLSPKSGSRVSVT 180
Qy 175 -----KAKNPQDSSLHMAAMALPALFSLITIGFAFGALYMKR 212
Db 181 KPFMLPVAASSLRNDSSSNRKAKNPQDSSLHMAAMALPALFSLITIGFAFGALYMKR 240
Qy 213 QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 245
Db 241 QPSLTRAVENTIOINEDNEISMLQEKEREFQEV 273

RESULT 12
US-08-336-728A-61
; Sequence 61, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-728a-61

Query Match 97.5%; Score 1231; DB 4; Length 273;
Best Local Similarity 89.4%; Pred. No. 4e-122;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKQTWTITCTIYQLLFNPLVKTGICRRNRYNNVDYTKLVANLPKDYMITLKYVPG 60
DB 1 MKQTWTITCTIYQLLFNPLVKTGICRRNRYNNVDYTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY 121 KDLKSFSPERPLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKDSRVSVT 180
QY 121 KDLKSFSPERPLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKDSRVSVT 180
QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAFGALYWKRR 212
DB 181 KPFMLPVAASSLRNDSSSNKAKNPPGDSLSHMAAMALPALFSLIIGFAFGALYWKRR 240
QY 213 QPSLTRAVENTIINEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIINEDNEISMLOEKEREFOEV 273

RESULT 13
US-08-482-918-48
Sequence 48, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-48

Query Match 97.1%; Score 1226; DB 4; Length 273;
Best Local Similarity 89.0%; Pred. No. 1.4e-121;
Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKQTWTITCTIYQLLFNPLVKTGICRRNRYNNVDYTKLVANLPKDYMITLKYVPG 60
DB 1 MKQTWTITCTIYQLLFNPLVKTGICRRNRYNNVDYTKLVANLPKDYMITLKYVPG 60
QY 61 MDVLPSCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQLSDSLTDLDFKFSNISEGLSNYSIIDKLVINIVDDLVECVKENS 120
QY 121 KDLKSFSPERPLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKDSRVSVT 180
QY 121 KDLKSFSPERPLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKDSRVSVT 180
DB 121 KDLKSFSPERPLFTPEEFRIKRSIDAFKDFVASETSDCVYSTLSPEKDSRVSVT 180
QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAFGALYWKRR 212
DB 181 KPFMLPVAASSLRNDSSSNKAKNPPGDSLSHMAAMALPALFSLIIGFAFGALYWKRR 240
QY 213 QPSLTRAVENTIINEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIINEDNEISMLOEKEREFOEV 273

RESULT 14
US-09-224-681-48
Sequence 48, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-48

Query Match
Best Local Similarity 97.1%; Score 1226; DB 4; Length 273;
Matches 243; Conservative 0; Mismatches 2; Indels 28; Gaps 1;

QY 1 MKQTQWILTCIYLLFNPVLTGEGICRNRYNNKVDYTKLVANLPKDYMTTLKYPG 60
DB 1 MKQTQWILTCIYLLFNPVLTGEGICRNRYNNKVDYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVINVDLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVINVDLVECVKENS 120
QY 121 KDLKSKFSPEPRLTPEEFRRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVST 174
DB 121 KDLKSKFSPEPRLTPEEFRRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVST 174
QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIGFAGALYWKRR 212
DB 181 KPEMLPPVAASSLRNDSSSNRKAAPGDSLSLHMAAMALPALFSLIGFAGALYWKRR 212
QY 213 QPSLTRAVENIQINEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENIQINEDNEISMLQEKEREFOEV 273

RESULT 15
US-08-482-918-50
Sequence 50, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsedeo, Kristzina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-50

Query Match
Best Local Similarity 96.3%; Score 1215; DB 4; Length 273;
Matches 241; Conservative 0; Mismatches 4; Indels 28; Gaps 1;

QY 1 MKQTQWILTCIYLLFNPVLTGEGICRNRYNNKVDYTKLVANLPKDYMTTLKYPG 60
DB 1 MKQTQWILTCIYLLFNPVLTGEGICRNRYNNKVDYTKLVANLPKDYMTTLKYPG 60
QY 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVINVDLVECVKENS 120
DB 61 MDVLPSCWISSEMYVQSLDLDLDFKFSNISEGLSNYSIIDKLVINVDLVECVKENS 120
QY 121 KDLKSKFSPEPRLTPEEFRRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVST 174
DB 121 KDLKSKFSPEPRLTPEEFRRIFNRSIDAFKDFVAVASSETSDCVSSTLSPKDSRVST 174
QY 175 -----KAKNPPGSSSLHMAAMALPALFSLIGFAGALYWKRR 212
DB 181 KPEMLPPVAASSLRNDSSSNRKAAPGDSLSLHMAAMALPALFSLIGFAGALYWKRR 212
QY 213 QPSLTRAVENIQINEDNEISMLQEKEREFOEV 245
DB 241 QPSLTRAVENIQINEDNEISMLQEKEREFOEV 273

Search completed: August 18, 2002, 13:04:02
Job time: 167 sec

Sun Aug 18 14:09:05 2002

us-09-604-325a-63.rai

Db 241 EFQEV 245

RESULT 2

A35974
 mast cell growth factor precursor - human
 N:Alternate names: kit ligand; stem cell factor
 C:Species: Homo sapiens (man)
 C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000
 C:Accession: A35974; A61190
 R:Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Tung, J.; Okino, K.H.; Morris, C.F.
 S; J.C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R.
 Cell 63; 203-211, 1990
 A:Title: Primary structure and functional expression of rat and human stem cell factor
 A:Reference number: A35974; MUID:91004219
 A:Accession: A35974
 A:Molecule type: mRNA
 A:Residues: 1-273 <MAR>
 A:Cross-references: GB:M59964; NID:g337933; PIDN:AAA85450.1; PID:g337934
 R:Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, I.
 Cell Growth Differ. 2, 373-378, 1991
 A:Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localized
 A:Reference number: A61190; MUID:9212791
 A:Accession: A61190
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-273 <AND>
 C:Genetics:
 A:Gene: GDB:MGP
 A:Cross-references: GDB:128026; OMIM:184745
 A:Map position: 12q22-12q22
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pro
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-273/Product: mast cell growth factor #status predicted <MCS>
 F:26-189/Product: (or 26-190) mast cell growth factor, soluble form #status predicted <M
 F:215-237/Domain: transmembrane #status predicted <TM>
 F:90,97,118,145,195/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.5%; Score 1231; DB 2; Length 273;
 Best Local Similarity 89.4%; Pred. No. 1,9e-92;
 Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNKRVNNKVDYKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNKRVNNKVDYKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPKSG----- 174
 Db 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPKSGRVSVT 180
 QY 175 -----KAKNPPGDSLSHMAALPALSLIIGFAFGALYKKR 212
 Db 181 KPFMLPVAASSLRNDSSSNRKANPPGDSLSHMAALPALSLIIGFAFGALYKKR 240
 QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
 Db 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 3
 c-kit ligand - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: 146575
 R:Zhang, Z.; Anthony, R.V.
 Biol. Reprod. 50, 95-102, 1994
 A:Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
 A:Reference number: 146575; MUID:94146218
 A:Accession: 146575

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-274 <ZHA>
 A:Cross-references: GB:L07786; NID:g164420; PIDN:AAA3670.1; PID:g164421
 C:Superfamily: mouse mast cell growth factor

Query Match 82.2%; Score 1037.5; DB 2; Length 274;
 Best Local Similarity 75.2%; Pred. No. 9.4e-77;
 Matches 206; Conservative 22; Mismatches 17; Indels 29; Gaps 2;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNKRVNNKVDYKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNKRVNNKVDYKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPKSG----- 174
 Db 121 ENVKSSKSPERLFTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPKSGRVSVT 180
 QY 175 -----KAKNPPGDSLSHMAALPALSLIIGFAFGALYKKR 211
 Db 181 TRPFLPVAASSLRNDSSSNRKASDSIEDSLQMAAVALPAFSLVIGFAFGALYKKR 240
 QY 212 ROPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
 Db 241 KOPNLTRAVENTIOINEDNEISMLOEKEREFOEV 274

RESULT 4

A37934
 mast cell growth factor precursor (version 2) - mouse
 N:Alternate names: KL-2 protein
 C:Species: Mus musculus (house mouse)
 C>Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
 C:Accession: A37934; B43751
 R:Flanagan, J.G.; Chan, D.C.; Leder, P.
 Cell 64, 1025-1035, 1991
 A:Title: Transmembrane form of the kit ligand growth factor is determined by alternat
 A:Reference number: A37934; MUID:91160046
 A:Accession: A37934
 A:Molecule type: mRNA
 A:Residues: 1-245 <FLA>
 A:Cross-references: GB:M64262
 R:Huang, E.J.; Nocke, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A:Title: Differential expression and processing of two cell associated forms of the k
 A:Reference number: A43751; MUID:92330001
 A:Accession: B43751
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-173, 'R', 175-186, 'L', 188-245 <HUA>
 A:Cross-references: GB:S04534
 A:Note: the authors translated the codon TTG for residue 187 as Trp
 C:Superfamily: mouse mast cell growth factor

Query Match 81.0%; Score 1022; DB 2; Length 245;
 Best Local Similarity 80.8%; Pred. No. 1.5e-75;
 Matches 198; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLLFNPLVKTGICRNKRVNNKVDYKLVANLPKDYMITLKYPG 60
 Db 1 MKKTQWILTCIYQLLLFNPLVKTGICRNKRVNNKVDYKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 Db 61 MDVLPSCWISSEMYVQLSDSLDLKFSNISEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSFSPERLFTPEEFRIFNRSIDAFKDFVVASSETSDCVVSTLSPKSGRVSVT 180

RESULT 6
I46929
stem cell factor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jul-2000
C:Accession: I46929
R:Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 1118-1124, 1992
A:Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic F
A:Reference number: I46929; MUID:33106145
A:Accession: I46929
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-274 <SHU>
A:Cross-references: GB:55329; NID:g262240; PIDN:AA824619.1; PID:g262241
C:Superfamily: mouse mast cell growth factor

RESULT 7
 565801
 mast cell growth factor - mouse
 M:Alternate names: hematopoietic growth factor KL; ligand steel factor; stem cell fac
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1996 #sequence-revision 27-Feb-1997 #text-change 01-Dec-2000
 C:Accession: S65801; A43751; A35976; A35972; A35975; A35973; 148768
 R:Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
 Genetics 142, 927-934, 1996
 A:Title: Multiple pathways for steel regulation suggested by genomic and sequence ana
 A:Reference number: S65801; MUID:97002551
 A:Accession: S65801
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-273 <BED>
 A:Cross-references: EMBL:U04725; NID:g1172215; PIDN:AMC52447.1; PID:g1172216
 R:Huang, E.-J.; Nocka, K.H.; Buck, J.; Besmer, P.
 Mol. Biol. Cell 3, 349-362, 1992
 A:Title: Differential expression and processing of two cell associated forms of the k
 A:Reference number: A43751; MUID:92330001
 A:Accession: A43751
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-214,'L', 216-273 <HUA>
 A:Cross-references: GB:S40364; NID:g251668; PIDN:AMB22554.2; PID:g5705957
 A:Note: the authors translated the codon TTG for residue 215 as Trp
 R:Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahn, H.W.; Wellner, D.; Le
 Cell 63, 225-233, 1990
 A:Title: The hematopoietic growth factor KL is encoded by the sl locus and is the lig
 A:Reference number: A35976; MUID:91004221
 A:Accession: A35976
 A:Status: preliminary: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-206,'S', 208-270 <HU2>
 A:Cross-references: GB:M38511
 R:Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; Mar
 Cell 63, 235-243, 1990
 A:Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active
 A:Reference number: A35977; MUID:91004223
 A:Accession: A35977
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-273 <AND>
 A:Cross-references: GB:M57647; GB:M34436; NID:g199151; PIDN:AAA39538.1; PID:g199152
 R:Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.;
 Cell 63, 175-183, 1990
 A:Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and
 A:Reference number: A35972; MUID:91004216

C:Species: Coturnix coturnix (quail)
C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Accession: S70367
R:Petite, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell factor
A:Reference number: S70366; MUID:96283808
A:Accession: S70367
A:Molecule type: mRNA
A:Residues: 1-253 <PEP>
A:Cross-references: EMBL:U03079; NID:g1150877; PIDN:AAC59934.1; PID:g1150878
C:Superfamily: mouse mast cell growth factor
C:Keywords: growth factor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-253/Product: stem cell factor short form #status predicted <MAT>
F:192-216/Domain: transmembrane #status predicted <TM>

Query Match	47.9%	Score 605;	DB 2;	Length 253;
Best Local Similarity	49.8%	Pred. No. 1e-41;		
Matches 126;	Conservative 48;	Mismatches 71;	Indels 8;	Gaps 5;
QY	1	MKKIQTWIIITCTIYDILLFNPLVKTEGICIRNVTNNKVDVTLVANI.PRDYMITLTKYVG	60	
Db	1	MKKAQTWIIITCTCIIOLLPLPLVKTOSCGNFPVTDVNDIAVLGNLPDVIITLTKYVPK	60	
QY	61	MDVLSHSCWISAMVYQSLSDFLDLDKF---SNIEGSLNSYSIDKLYNIYDDLYEVCYKE	117	
Db	61	MDSLPNCWHLHMAVEFRSLSHNLQKRYVDSDMSDVLNSNIIINLIRIINDIMACAKF	120	
QY	118	NSSKC-LKSKSEKPEPRLLTFPEEFERFIRNRSIDAKRFVVASETSDCVYVSFTL-SPEKGG	175	
Db	121	DKNKQFIEINGHLVEDDFRIFIEPNEFRLLNRTIEYKKEPADSLDKNDCIMPSTVEPRPENE	180	
QY	176	AKNPFGDSSILHMAAVALRALPSLITIGFAFGALYMKKKRP-SITRAVENIQIN--EDENET	232	
Db	181	ALGFSSSSSLGIGIALSLSLSLSLGLGVLGYIYMAKTHPKSPRESNETTQCHGQEEENET	240	
QY	233	SMLOEKEREFOEY 245		
Db	241	SMLOEKEREHLOY 253		

```

RESULT      11
JN0637
stem cell factor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0637
R:Zhou, J.H.; Ontak, M.; Sakurai, M.
Gene 127, 269-270, 1993
A:Title: Sequence of a cDNA encoding chicken stem cell factor.
A:Reference number: JN0637; MID:9373244
A:Accession: JN0637
A:Molecule type: mRNA
A:Residues: 1-287 <ZHO>
A:Cross-references: GB:13516; NID:g391646; PIDN:BAA02733.1; PID:g391649
A:Experimental source: brain
C:Superfamily: mouse mast cell growth factor
F:1-25/Domain1: signal sequence #status predicted <SIG>
F:26-287/Product: stem cell factor #status predicted <MAT>
F:226-248/Domain1: transmembrane #status predicted <TM>

```

Query Match	46.3%	Score 584	DB 2	Length 287
Best Local Similarity	44.6%	Pred No. 6	le 4%	
Matches 128	Conservative 46	Mismatches 71	Indels 42	Gaps 7
1	MKTKTQMIILCIITLITLLEPNPLVETGECICRNRVNNKADYTKLVANLPKDYMTTEKRVG	60		
1	MKKAGVMIITICFGLQLLINPLNPLVKAQSSCGNEPVDVNDLAKLVGINLPNDYLTTEKTVYKR	60		

```
QY      61 MDVESHQMISMWVOYLSDSLTDLLDKRSNT---SEGLSNSTIIDKLNVYDVLVECYKE 117
       |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      61 MDSLEPHCHWHLAMPERSKSLAHNLNKKLQSDMSDVLSNITNNLTRIINDMLCLAP 120
QY      118 NSSKD-LKSKSRSPPEPLTFTEPEEFRIFNRSIDAFCDFVAASETDCVVSSTL-SPKRGK 175
       :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      121 DKNKFIEIKENGHLYEEDRFIDENFRIFLNFTIERYKFEAFSLDKNCIMSTIETEPENDS 180
QY      176 -----AKNP-----GSSSLHWAMALPALFSLIG 201
       |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      181 RAAVATRTISFPVPAASSLRNDISGSNTSSNSNKKEALGFISSSTHGQISIALTLFLSLIG 240
QY      202 FAFGLKYRKROP-SLTGRAVENIOIN--EDNEISMLOEKREPEROEY 245
       |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      241 FILGAIYWKTHPKRSREPNETTIQHCQCKEENESIMLOQCKEHDIQY 287
```

RESULT 12
 S70366
 stem cell factor long form precursor - quail
 C:Species: *Coturnix coturnix* (quail)
 C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
 C:Accession: S70366
 R:Petitte, J.N.; Kulik, M.J.
 Biochim. Biophys. Acta 1307, 149-151, 1996
 A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell
 A:Reference number: S70366; M0ID:96283808
 A:Accession: S70366
 A:Molecule type: mRNA
 A:Residues: 1-287 <PEP>
 A:Cross-references: EMBL:U43078; NID:g1150875; PIDD:AAc59933.1; PID:g1150876
 C:Superfamily: mouse mast cell growth factor
 C:Keywords: growth factor; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <Sig>
 F:26-287/Product: stem cell factor long form #status predicted <NAF>
 F:126-250/Domain: transmembrane #status predicted <TMM>

Query March Best Local Similarity Matches	46.2% 44.3% 127;	Score 583; Pred. No. 7.4e-40; Conservative 47;	DB 42; Mismatch 71; Indels 42;	Length 287; Gaps
QY	1	MKKQTQWILTCIYLQLLFNPLVKTGICRRRVNANNKDYTKLVANLPKDYMITLTKYPG	60	
Db	1	MKKQQTWIIIFCFQCLLLPLNPLVKTQSSCGNPYDIDVNDIAKLGVNLPMNDYITLITLKYPK	60	
QY	61	MDVLPSCHWISEWVYVQDLSLTDLLDKF---SNTSELSMYSTIIDLKLVINVDVLECYKE	117	
Db	61	MDSLPNCWMLHLYAPFSSLSLNLLOKRVQDLSIDSDVLSNLTINNLRTINDIMACIATF	120	
QY	118	NSSD--LKSSFSFSPERLFTPEEFRIIFNRSIDAFDEVASFTSDCVVSSYTL--SPEKGK	177	
Db	121	DKNKDKFTKEGHLIYEDRITPEINFEFRLEFNRTIIEYKEFAFDASLDKNCIDCIMPSTVEPENDS	180	
QY	176	-----AKNP-----		
Db	181	RVAVTITSEPPVYASSLRNDSIGSNSSNKKKALGFISSSLGISTALSTLSTLSTLG	201	
QY	202	FAGGALYMKRKP--SLTRAIVENIQTN--EEDNEISMLQEKEREFOEY	245	
Db	241	FILGVLYMKRTHPKSPSPSNTTQCHCGOEBENISMLQEKREHIOY	287	

```

RESULT      13
S29052
stem cell factor - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: S29052
R:Lin, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderak, K.; Balter
Arch. Biochem. Biophys. 298, 150-158, 1992
Title: Post-translational processing of membrane-associated recombinant human stem

```

A:Reference number: S29052; MUID:92398336

A:Accession: S29052

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>

C:Superfamily: mouse mast cell growth factor

Query Match

Best Local Similarity 38.9%; Score 491.5; DB 2; Length 124;
Matches 107; Conservative 0; Mismatches 0; Indels 41; Gaps 4;

OY 26 EICRNRYTNVKKDYTKLVANLPKDYMTLLKYPGMDVLPSCWISSEMYVQLS-----DVLPSHCWISSEMYVQLS----- 30

DB 1 EICRNRYTNVKKDYTKLVANLPKDYMTLLKYPGMDVLPSCWISSEMYVQLS-----DVLPSHCWISSEMYVQLS----- 30

OY 86 DKFSNISSEGLSNYSITIDKLVNIVDDLVKCKENSSKDLKSKSPKSPRLFTPEEFRIEN 145

DB 31 DKFSNISSEGLSNYSIT-----DDLVECKENSSKDLKSKSPKSPRLFTPEEFRIEN 83

OY 146 RSIDAFKDFVAVSETSDCVSSTLSPEK 173

DB 84 RSI-----DFVAVSETSDCVSSTLSPEK 107

RESULT 14

B35971

mast cell growth factor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000

C:Accession: B35971

R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.

Cell 63, 167-174, 1990

A:Title: Identification of a ligand for the c-kit proto-oncogene.

A:Reference number: A35971; MUID:91004215

A:Accession: B35971

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-51 <WIL>

C:Superfamily: mouse mast cell growth factor

C:Keywords: transmembrane protein

Query Match 13.9%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 9e-08; 7; Indels 1; Gaps 1;

Matches 34; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

OY 28 ICRNRYTNVKKDYTKLVANLPKDYMTLLKYPGMDVLPSCWISSEMY 74

DB 3 ICRNRYTNVKKDYTKLVANLPKDYMTLLKYPGMDVLPSCWISSEMY 74

RESULT 15

mast cell growth factor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 21-Jul-2000

C:Accession: A35971

R:Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.

Cell 63, 167-174, 1990

A:Title: Identification of a ligand for the c-kit proto-oncogene.

A:Reference number: A35971; MUID:91004215

A:Accession: A35971

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-49 <WIL>

C:Superfamily: mouse mast cell growth factor

C:Keywords: transmembrane protein

Query Match 13.7%; Score 172.5; DB 2; Length 49;
Best Local Similarity 73.5%; Pred. No. 1.5e-07; 6; Indels 3; Gaps 2;

Matches 36; Conservative 4; Mismatches 6; Indels 3; Gaps 2;

OY 28 ICRNRYTNVKKDYTKLVANLPKDYMTLLKYPGMDVLPSCWISSEMYVQ 76

DB 3 ICRNRYTNVKKDYTKLVANLPKDYMTLLKYPGMDVLPSCWISSEMYVQ 76

Search completed: August 18, 2002, 13:03:16
Job time: 121 sec

Sun Aug 18 14:09:06 2002

us-09-604-325a-63.rpt

1

2

3

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 13:02:07 ; Search time 35.93 Seconds

(without alignments)
264.021 Million cell updates/sec

Title: US-09-604-325a-63

Perfect score: 1262

Sequence: 1 MKKTQTWILTCIYQLLEFN.....NEEDNEISMLQEKEREFQEV 245

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1231	97.5	273	1	SCF_HUMAN
2	1037.5	82.2	274	1	SCF_PIG
3	1014.5	80.4	274	1	SCF_CANFA
4	991	78.5	273	1	SCF_MOUSE
5	721	57.1	201	1	SCF_RAT
6	584	46.3	287	1	SCF_CHICK
7	97	7.7	482	1	T2PA_YEAST
8	94.5	7.5	403	1	RAGE_MOUSE
9	91	7.2	378	1	PDHA_METVA
10	91	7.2	402	1	RAGE_RAT
11	91	7.2	981	1	SCA4_RICPE
12	90.5	7.2	1675	1	PKI_NPVH
13	90	7.1	267	1	PKI_NPVH
14	90	7.1	411	1	RMOC_CHLBN
15	89	7.1	2238	1	RRL_BUNYW
16	88	7.0	447	1	DNAA_SYX3
17	87.5	6.9	966	1	CAPR_MEDSA
18	87.5	6.9	1175	1	SRS2_YEAST
19	87	6.9	664	1	NRF_CAEEL
20	86.5	6.9	370	1	NRF_HAELN
21	86.5	6.9	2492	1	TAIA_DICDI
22	86	6.8	469	1	C39A_HUMAN
23	86	6.8	1146	1	KMAA_DICDI
24	85	6.7	804	1	SUS2_ARATH
25	85	6.7	953	1	IVRA_RICPR
26	85	6.7	1188	1	PPSA_METVA
27	84.5	6.7	466	1	DNAA_PROMI
28	84.5	6.7	1075	1	CAPR_TOBAC
29	84.5	6.7	1075	1	PST2_SCHPO
30	84.5	6.7	2156	1	RPL_HUMAN
31	84	6.7	935	1	COPG_YEAST
32	84	6.7	935	1	Y31_YEAST
33	84	6.7	1224	1	MSN5_YEAST

34	84	6.7	1522	1	BA13_HUMAN	060242 homo sapien
35	83.5	6.6	456	1	DNA1_CHLTR	084252 chlamydia t
36	83.5	6.6	796	1	DECI_YEAST	012387 saccharomyc
37	83.5	6.6	830	1	EP2_DICDI	P15112 dictyostell
38	83.5	6.6	998	1	SCA4_RICAK	09a1x9 rickettsia
39	83.5	6.6	1742	1	MYSC_HUMAN	09nq4 homo sapien
40	83	6.6	989	1	PTP3_DICDI	P54637 dictyostell
41	83	6.6	1584	1	BA11_HUMAN	014514 homo sapien
42	82.5	6.5	425	1	YNU7_YEAST	P40160 saccharomyc
43	82.5	6.5	450	1	DNAA_SPICI	P34028 spiroplasma
44	82.5	6.5	451	1	DNAA_PASMT	09c1q4 pasteurella
45	82.5	6.5	463	1	DNAA_PROS9	09a247 prochlorococ

ALIGNMENTS

RESULT 1	SCF_HUMAN	STANDARD:	PRT:	273 AA.
ID	P21583;			
AC	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast cell growth factor) (MGF).			
GN	KitLG OR MGF OR SCF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91004219; PubMed=2208279;			
RA	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,			
RA	Morris C.F., McNice I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,			
RA	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,			
RA	Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,			
RA	Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.,			
RT	"Primary structure and functional expression of rat and human stem cell factor DNAs."			
RL	Cell 63:203-211(1990).			
CC	-1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.			
CC	-1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLY).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.			
CC	-1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.			
CC	-1- SIMILARITY: BELONGS TO THE SCF FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: M59964; AAA85450.1; -			
DR	PIR: A35974; A35974.			
DR	MIM: 184745; -			
DR	InterPro: IPR003452; SCF.			
DR	Pfam: PF02404; SCF: 1.			
KW	Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.			
FT	SIGNAL	1	25	
FT	CHAIN	26	273	KIT LIGAND.
FT	DOMAIN	26	214	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	215	237	POTENTIAL.
FT	DOMAIN	238	273	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	29	114	BY SIMILARITY.

Query Match 97.5%; Score 1231; DB 1; Length 273;
Best Local Similarity 89.4%; Pred. No. 2.4e-91;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

FT DISULFID 68 163 BY SIMILARITY.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 273 AA; 30898 MW; 19FD362CB39C6607 CRC64;

Query Match 97.5%; Score 1231; DB 1; Length 273;
Best Local Similarity 89.4%; Pred. No. 2.4e-91;
Matches 244; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

DB 1 MKKTQWIIITCIYQLLLFNPVLTGEGICNNRVYNNKVDYTKLVANLPKDYMTITLKYPG 60
DB 1 MKKTQWIIITCIYQLLLFNPVLTGEGICNNRVYNNKVDYTKLVANLPKDYMTITLKYPG 60
QY 1 MKKTQWIIITCIYQLLLFNPVLTGEGICNNRVYNNKVDYTKLVANLPKDYMTITLKYPG 60
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
QY 121 KDLKSEKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVYSTLSPEKG----- 174
DB 121 KDLKSEKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVYSTLSPEKG----- 180
QY 175 -----KAKNPGDSSLHMAAALPALFSLIIGFAFGALYWK 212
DB 181 KPFMLPYVAASSLRNDSSSNRKAHPGDSLLHMAAALPALFSLIIGFAFGALYWK 240
QY 213 QPSLTRAVENTIQUINEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIQUINEDNEISMLOEKEREFOEV 273

RESULT 2
SCF_PIG 2
ID SCF_PIG STANDARD; PRT; 274 AA.
AC 029030:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
GN KITLG OR MGF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RX MEDLINE-94146218; PubMed=7508758;
RA Zhang Z., Anthony R.V.;
RT "Porcine stem cell factor/c-kit ligand: its molecular cloning and localization within the uterus.";
RL Biol. Reprod. 50:95-102(1994).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A SECRETED SOLUBLE FORM.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
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Query Match 82.2%; Score 1037.5; DB 1; Length 274;
Best Local Similarity 75.2%; Pred. No. 6.7e-76;
Matches 206; Conservative 22; Mismatches 17; Indels 29; Gaps 2;

DR EMBL; L07786; AAA53670.1; -
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 274 KIT LIGAND.
FT DOMAIN 26 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 POTENTIAL.
FT DISULFID 239 274 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 29 114 BY SIMILARITY.
FT DISULFID 29 114 BY SIMILARITY.
FT CARBOHYD 68 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 274 AA; 31118 MW; FE3C8711AD7BA666 CRC64;

Query Match 82.2%; Score 1037.5; DB 1; Length 274;
Best Local Similarity 75.2%; Pred. No. 6.7e-76;
Matches 206; Conservative 22; Mismatches 17; Indels 29; Gaps 2;

QY 1 MKKTQWIIITCIYQLLLFNPVLTGEGICNNRVYNNKVDYTKLVANLPKDYMTITLKYPG 60
DB 1 MKKTQWIIITCIYQLLLFNPVLTGEGICNNRVYNNKVDYTKLVANLPKDYMTITLKYPG 60
QY 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
DB 61 MDVLPSCWISSEWVQSDSLTDLDFKFSNISEGLSNYSIIDKLVIYVDLVECKENSS 120
QY 121 KDLKSEKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVYSTLSPEKG----- 174
DB 121 KDLKSEKSPERLFTPEEFRIFNRSIDAFKDFVVASETSDCVYSTLSPEKG----- 180
QY 175 -----KAKNPGDSSLHMAAALPALFSLIIGFAFGALYWK 212
DB 181 KPFMLPYVAASSLRNDSSSNRKAHPGDSLLHMAAALPALFSLIIGFAFGALYWK 240
QY 212 QPSLTRAVENTIQUINEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIQUINEDNEISMLOEKEREFOEV 274

RESULT 3
SCF_CANFA 3
ID SCF_CANFA STANDARD; PRT; 274 AA.
AC 006220:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
GN KITLG OR MGF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedidae; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE-93106145; PubMed=1281786;
RA Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W., Martin F.H.;
RT "Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture.";
RL Exp. Hematol. 20:1118-1124(1992).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES, PROBABLY INTERLEUKINS.
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC or send an email to license@isb-sib.ch).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S53329; AAB24619.1; -
 CC DR InterPro: IPR003452; SCF.
 CC Pfam: PF02404; SCF. 1.
 CC Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 KW Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
 FT SIGNAL 1 25
 FT CHAIN 1 25
 FT DOMAIN 26 274
 FT TRANSSEM 26 215
 FT DOMAIN 216 238
 FT DISULFID 239 274
 FT DISULFID 29 114
 FT DISULFID 68 164
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 196 196
 SQ SEQUENCE 274 AA; 30869 MW; 4182BE9AED0073B CRC64;

Query Match 80.4%; Score 1014.5; DB 1; Length 274;
 Best Local Similarity 74.8%; Pred. No. 4.6e-74;
 Matches 205; Conservative 17; Mismatches 23; Indels 29; Gaps 2;

QY 1 MKKTQWILNCITQLLLFNPVKTEICGRNNTNNKVDTKYANLPKDYMTTLKYVG 60
 Db 1 MKKTQWILNCITQLLLFNPVKTEICGRNNTNNKVDTKYANLPKDYMTTLKYVG 60
 QY 61 MDVLPSCWISWVYVDSLDLDFKSNISGLSNYSITDKLVNIYVDLVCEVKNES 120
 Db 61 MDVLPSCWISWVYVDSLDLDFKSNISGLSNYSITDKLVNIYVDLVCEVKNES 120
 QY 121 KDLKSKSPERLPTPEEFRRFNSSDAKDF-VVASETSDCVVSTLSPKRG----- 174
 Db 121 ENVKKAPKSELPKLPPEEFRRFNSSDAKDF-VVASETSDCVVSTLSPKRG----- 180
 QY 175 -----KAKNPQDSSLHMAAMALPALSLLIGFAGALYMKK 211
 Db 181 TKPFMLPYVAASLRLNDSSSNKASNSIGDSMLQMAAMALPALSLLIGFAGALYMKK 240
 QY 212 RQPSLRLAVENIOINEDNEISMLOEKEREFOEV 245
 Db 241 KQPNLRLTVENIOINEDNEISMLOEKEREFOEV 274

RESULT 4
 SCF_MOUSE STANDARD; PRT; 273 AA.
 AC P20826;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
 DE cell growth factor) (MGF) (Hematopoietic growth factor KL) (KL-1
 DE protein) (Steel factor).
 GN KITLG OR KITL OR MGF OR SL OR SLF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=WCB6F1;
 RX MEDLINE=91004223; PubMed=1698558;
 RA Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
 RA Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D.,
 RA Williams D.E.;
 RT "Molecular cloning of mast cell growth factor, a hematopoietin that
 RT is active in both membrane bound and soluble forms.";
 RL Cell 63:235-243(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92330001; PubMed=1378327;
 RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
 RT "Differential expression and processing of two cell associated forms
 RT of the kit-ligand: KL-1 and KL-2.";
 RL Mol. Biol. Cell 3:349-362(1992).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=WCB6F1;
 RX MEDLINE=91160046; PubMed=1705866;
 RA Flanagan J.G., Chan D.C., Leder P.;
 RT "Transmembrane form of the kit ligand and growth factor is determined by
 RT alternative splicing and is missing in the Sld mutant.";
 RL Cell 64:1025-1035(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93012940; PubMed=1383087;
 RA Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
 RA Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A.,
 RA Copeland N.G.;
 RT "Developmental abnormalities in Steel17H mice result from a splicing
 RT defect in the steel factor cytoplasmic tail.";
 RL Genes Dev. 6:1832-1842(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=97002551; PubMed=8849898;
 RA Bedell M.A., Copeland N.G., Jenkins N.A.;
 RT "Multiple pathways for Steel regulation suggested by genomic and
 RT sequence analysis of the murine Steel gene.";
 RL Genetics 142:927-934(1996).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=(102/ELX3H/EL)F1; TISSUE=Brain;
 RA Gray J.;
 RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 1-270 FROM N.A., AND SEQUENCE OF 26-65.
 RX MEDLINE=91004221; PubMed=1698557;
 RA Huang E., Nocka K., Beier D.R., Chu T.Y., Buck J., Lahm H.W.,
 RA Wellner D., Leder P., Besmer P.;
 RT "The hematopoietic growth factor KL is encoded by the Sl locus and is
 RT the ligand of the c-kit receptor, the gene product of the W locus.";
 RL Cell 63:225-233(1990).
 RN [8]
 RP SEQUENCE OF 1-201 FROM N.A.
 RX MEDLINE=91004220; PubMed=1698556;
 RA Zsebo K.M., Williams D.A., Geissler E.N., Broudy V.C., Martin F.H.,
 RA Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Murodock D.C.,
 RA Jacobsen P.W., Langley K.E., Smith K.A., Takeishi T., Cattanech B.M.,
 RA Galli S.J., Sugis S.V.;
 RT "Stem cell factor is encoded at the Sl locus of the mouse and is the
 RT ligand for the c-kit tyrosine kinase receptor.";
 RL Cell 63:213-224(1990).
 RN [9]
 RP SEQUENCE OF 26-53.
 RX MEDLINE=91004216; PubMed=1698554;
 RA Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,
 RA Cosman D., Anderson D., Lyman S.D., Williams D.E.;
 RT "Mast cell growth factor maps near the steel locus on mouse
 RT chromosome 10 and is deleted in a number of steel alleles.";
 RL Cell 63:175-183(1990).
 RN [10]
 RP PARTIAL SEQUENCE OF 26-78.

RX MEDLINE=91004215; PubMed=1698553;
 RA Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K.,
 RA Burgess C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S.,
 RA Burgess G.S., Cosman D., Lyman S.D.;
 RT "Identification of a ligand for the c-kit proto-oncogene."
 RL Cell 61:167-174(1990).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.
 CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVELY SPLICED FORMS DIFFERING BY
 CC THE PRESENCE OR ABSENCE OF EXON 6 HAVE BEEN OBSERVED AND OCCUR IN
 CC VARYING RATIOS IN DIFFERENT TISSUES.
 CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
 CC -1- PTM: THE LONG FORM APPEARS TO CONTAIN A PROTEOLYTIC CLEAVAGE SITE
 CC ENCODED BY EXON 6 SUCH THAT THE ACTIVE REGION OF THE EXTRACELLULAR
 CC DOMAIN IS RELEASED FROM THE MEMBRANE IN A SOLUBLE FORM.
 CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M59915; AAA40095.1; -;
 DR EMBL; M57647; AAA39538.1; -;
 DR EMBL; X68989; CAA48778.1; -;
 DR EMBL; U44724; -; NOT_ANNOTATED_CDS.
 DR EMBL; U44725; AAC52447.1; -;
 DR EMBL; X95381; CAA64667.1; -;
 DR EMBL; S40364; AAB22554.2; -;
 DR EMBL; M59912; AAA39539.1; -;
 DR PIR; A35971; A35971.
 DR PIR; A35972; A35972.
 DR PIR; A35975; A35975.
 DR PIR; A35976; A35976.
 DR PIR; A35977; A35977.
 DR PIR; A43751; A43751.
 DR PIR; B35971; B35971.
 DR MGI; MGI:96974; KILL.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF; 1.
 KW Growth factor; Glycoprotein; Transmembrane; Signal;
 KW Alternative splicing; Cell adhesion.
 FT SIGNAL 1 25
 FT CHAIN 26 273
 FT DOMAIN 26 214
 FT TRANSMEM 215 237
 FT DOMAIN 238 273
 FT DISULFID 29 114
 FT DISULFID 68 163
 FT CARBOHYD 90 90
 FT CARBOHYD 97 97
 FT CARBOHYD 145 145
 FT CARBOHYD 145 145
 FT CARBOHYD 195 195
 FT VARSPLIC 175 202
 FT VARIANT 207 215
 FT VARIANT 215 215
 FT CONFLICT 215 215
 FT SEQUENCE 273 AA; 30645 MW; A7FC89B592A7967 CMC64;

Query Match 78.5%; Score 991; DB 1; Length 273;
 Best Local Similarity 72.2%; Pred. No. 3.4e-72;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

1 MKKTQWTLCTIYLLLFNPLVKTGICRNRVYTNNAVDTKLVANLFRDVIITLIKYPG 60

DB 1 MKKTQWTLCTIYLLLFNPLVKTGICRNRVYTNNAVDTKLVANLFRDVIITLIKYPG 60
 OY 61 MDVLPSSHCWISWVYQSDSLTDLDFKSNISELSNYITDKLVNIVYDVLVEKSNSS 120
 DB 61 MDVLPSSHCWISWVYQSDSLTDLDFKSNISELSNYITDKLVNIVYDVLVEKSNAP 120
 OY 121 KDIKFSKSPPEPLFTPEEPFRINRSIDAFKDPVVASETSDCVSVSTLSPKNG----- 174
 DB 121 KNIKSPRPETRSTFTPEEFSTNRSIDAKDPVVAASDTSDCVLSSTLGPCKSRVSVT 180
 OY 175 -----KAKNPPGSSLHWAMALPALFSLITGFAFGALYKKR 212
 DB 181 KPFLPVAASSLRNDSSSSNRKAKAPEDSGLOMTAMALPALISIVIGFAFGALYKKR 240
 OY 213 OPSLTRAVENTIOINEDNEIMSLCKEKEPEOV 245
 DB 241 OSLLTRAVENTIOINEDNEIMSLCKEKEPEOV 273
 RESULT 5
 SCF_RAT STRAND: PRT: 201 AA.
 AC P21581;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE kit ligand precursor (C-kit ligand) (stem cell factor) (SCF) (Mast
 DE cell growth factor) (MCF) (Fragment).
 GN KITLG OR MGF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=91004219; PubMed=2208279;
 RA Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
 RA Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birckett N.C.,
 RA Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
 RA Fisher E.F., Ertvec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
 RA Pope J.A., Leslie I., Men D., Lin C.-H., Cupples R.L., Zsebo K.M.;
 RT Primary structure and functional expression of rat and human stem
 RT cell factor DNAs.
 RL Cell 63:203-211(1990).
 RN [2]
 RP SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RC STRAIN=BUFALO; TISSUE=Liver;
 RX MEDLINE=91217037; PubMed=1708771;
 RA Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
 RA Mendiaz E.A., Zsebo K.M., Langley K.E.;
 RT Amino acid sequence and post-translational modification of stem cell
 RT factor isolated from buffalo rat liver cell-conditioned medium.
 RL J. Biol. Chem. 266:8102-8107(1991).
 RN [3]
 RP SEQUENCE OF 26-39.
 RX MEDLINE=91004218; PubMed=2208278;
 RA Zsebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A.,
 RA Karikari S.B., Sachdev R.K., Yushchenko V.N., Birckett N.C.,
 RA Williams L.R., Satyagal V.N., Tung W., Bosseman R.A., Mendiaz E.A.,
 RA Langley K.E.;
 RT Identification, purification, and biological characterization of
 RT hematopoietic stem cell factor from buffalo rat liver-conditioned
 RT medium.
 RL Cell 63:195-201(1990).
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
 CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
 CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
 CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,
 CC PROBABLY INTERLEUKINS.
 CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
 CC SECRETED SOLUBLE FORM.


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CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -----
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CC -----
CC DR EMBL; M59966; AAA42117.1; -.
CC DR PIR; B35974; B35974.
CC DR PIR; A35973; A35973.
CC DR InterPro; IPR003452; SCF.
CC DR Pfam; PF02404; SCF; 1.
CC
CC Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
CC
CC FT CHAIN 1 25
CC FT MOD_RES 26 >201 KIT LIGAND.
CC FT DISULFID 29 114 PYROLIDONE CARBOXYLIC ACID.
CC
CC FT CARBOHYD 68 163
CC FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (PARTIAL).
CC FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) .
CC FT CARBOHYD 167 167 O-LINKED (PROBABLE).
CC FT CARBOHYD 168 168 O-LINKED (PROBABLE).
CC FT CARBOHYD 180 180 O-LINKED (PROBABLE).
CC FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (PARTIAL).
CC FT NON_TER 201
CC
CC SEQUENCE 201 AA; 22537 MW; 188868C1DA4F21B CRC64;

Query Match 57.1%; Score 721; DB 1; Length 201;
Best Local Similarity 79.8%; Pred. No. 8.5e-51;
Matches 138; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRYTNVNDVYKLVANLPDVMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRYTNVNDVYKLVANLPDVMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLDLDFKFSNISSEGLSNYSIIDKLVNIYDDIVECKENS 120
DB 61 MDVLPSCWISSEWVQVLSLDLDFKFSNISSEGLSNYSIIDKLVNIYDDIVECKENS 120
QY 121 KDLKRSKSPERLTPPEPFRIIFNRSIDAFKDVVASTSCVVSSTLSPK 173
DB 121 KDLKRSKSPERLTPPEPFRIIFNRSIDAFKDVVASTSCVVSSTLSPK 173
QY 121 KNNKESLAKRETNPTEPFRIIFNRSIDAFKDVVASTSCVVSSTLSPK 173
DB 121 KNNKESLAKRETNPTEPFRIIFNRSIDAFKDVVASTSCVVSSTLSPK 173

RESULT 6
SCF_CHICK
ID SCF_CHICK STANDARD; PRT; 287 AA.
AC 009108;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
DE cell growth factor) (MCF).
GN KITLG.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93373244; PubMed=7684722;
RA Zhou J., Ohtaki M., Sakurai M.;
RT "Sequence of a cDNA encoding chicken stem cell factor.";
RL Gene 127:269-270(1993).
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF MAST CELLS. ABLE TO
CC AUGMENT THE PROLIFERATION OF BOTH MYELOID AND LYMPHOID
CC HEMATOPOIETIC PROGENITORS IN BONE MARROW CULTURE. MEDIATES ALSO
CC CELL-CELL ADHESION. ACTS SYNERGISTICALLY WITH OTHER CYTOKINES,

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```

CC PROBABLY INTERLEUKINS.
CC -1- SUBUNIT: HOMODIMER, NON-COVALENTLY LINKED (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SECRETED SOLUBLE FORM.
CC -1- DEVELOPMENTAL STAGE: ACTS IN THE EARLY STAGES OF HEMATOPOIESIS.
CC -1- SIMILARITY: BELONGS TO THE SCF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; D13516; BAA02733.1; -.
CC DR PIR; JN0637; JN0637.
CC DR InterPro; IPR003452; SCF.
CC DR Pfam; PF02404; SCF; 1.
CC
CC Growth factor; Glycoprotein; Transmembrane; Signal; Cell adhesion.
CC
CC FT CHAIN 1 25
CC FT MOD_RES 26 >201 KIT LIGAND.
CC FT DISULFID 29 117 POTENTIAL.
CC
CC FT CARBOHYD 68 167 EXTRACELLULAR (POTENTIAL).
CC FT CARBOHYD 100 100 POTENTIAL.
CC FT CARBOHYD 149 149 POTENTIAL.
CC FT CARBOHYD 200 200 POTENTIAL.
CC
CC SEQUENCE 287 AA; 32328 MW; 6A8556AD0C152578 CRC64;

Query Match 46.3%; Score 584; DB 1; Length 287;
Best Local Similarity 44.6%; Pred. No. 1.1e-39;
Matches 128; Conservative 46; Mismatches 71; Indels 42; Gaps 7;

QY 1 MKKTQWILTCIYQLLEFNPVKTGICRNRYTNVNDVYKLVANLPDVMITLKYPG 60
DB 1 MKKTQWILTCIYQLLEFNPVKTGICRNRYTNVNDVYKLVANLPDVMITLKYPG 60
QY 61 MDVLPSCWISSEWVQVLSLDLDFKFSNI--SEGLSNYSIIDKLVNIYDDIVECKE 117
DB 61 MDVLPSCWISSEWVQVLSLDLDFKFSNI--SEGLSNYSIIDKLVNIYDDIVECKE 117
QY 61 MDVLPSCWISSEWVQVLSLDLDFKFSNI--SEGLSNYSIIDKLVNIYDDIVECKE 117
DB 61 MDVLPSCWISSEWVQVLSLDLDFKFSNI--SEGLSNYSIIDKLVNIYDDIVECKE 117
QY 118 NSSKD-LKRSKSPERLTPPEPFRIIFNRSIDAFKDVVASTSCVVSSTLSPK 175
DB 118 NSSKD-LKRSKSPERLTPPEPFRIIFNRSIDAFKDVVASTSCVVSSTLSPK 175
QY 121 KNNKESLAKRETNPTEPFRIIFNRSIDAFKDVVASTSCVVSSTLSPK 173
DB 121 KNNKESLAKRETNPTEPFRIIFNRSIDAFKDVVASTSCVVSSTLSPK 173
QY 176 -----AKNP-----GDSIHMAMALPAFLSLIG 201
DB 176 -----AKNP-----GDSIHMAMALPAFLSLIG 201
QY 181 RYAVNTKISFPYVASSLRNDSIGSNTSSNKKELGFISSSLQGISALTSLSLIG 240
DB 181 RYAVNTKISFPYVASSLRNDSIGSNTSSNKKELGFISSSLQGISALTSLSLIG 240
QY 202 FAFGALYMKKROP-SITRAVENIQIN--EDNEISMLQEKREFOEV 245
DB 202 FAFGALYMKKROP-SITRAVENIQIN--EDNEISMLQEKREFOEV 245
QY 241 FIFGALYMKKTHPKSPRESNETIQCHGQENEISMLQEKREHLY 287
DB 241 FIFGALYMKKTHPKSPRESNETIQCHGQENEISMLQEKREHLY 287

RESULT 7
T2EA_YEAST
ID T2EA_YEAST STANDARD; PRT; 482 AA.
AC P36100;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription initiation factor IIF, alpha subunit (TIF1E-alpha)
DE (Transcription factor A large subunit) (Factor A 66 kDa subunit).
GN TFI1 OR YKL028W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN (1)

```

RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-71; 102-108 AND 206-220.
 RC STRAIN-BJ926;
 RX MEDLINE=95050500; PubMed=7961670;
 RA Feaver W.J., Henry N.L., Bushnell D.A., Sayre M.H., Brickner J.H.,
 RA Gillead O., Kornberg R.D.,
 RT "yeast TFIIE. Cloning, expression, and homology to vertebrate
 RT proteins";
 RL J. Biol. Chem. 269:27549-27553(1994).
 RN
 RP SEQUENCE FROM N.A.
 RA Rieger M.,
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECRUITS TFIIF TO THE INITIATION COMPLEX AND STIMULATES
 CC THE RNA POLYMERASE II C-TERMINAL DOMAIN KINASE AND DNA-DEPENDENT
 CC ATPASE ACTIVITIES OF TFIIF. BOTH TFIIF AND TFIIE ARE REQUIRED FOR
 CC PROMOTER CLEARANCE BY RNA POLYMERASE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: STRONG, TO MAMMALIAN TFIIE-ALPHA.
 CC
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 CC
 CC EMBL: U12825; AAA62665.1; -
 DR EMBL: Z28028; CAA81863.1; -
 DR PIR: S37845; S37845.
 DR TRANSFAC: T02239; -
 DR SGD: S0001511; TEAF.
 DR InterPro: IPR002853; TFIIF_alpha.
 DR Pfam: PF02002; TFIIE_alpha.1.
 DR SMART: SM00531; TFIIE_alpha.1.
 DR Transcription regulation; Nuclear protein; Zinc-finger.
 KW ZN_FING 124 152
 FT DOMAIN 374 482 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 374 392 POLY-GLU
 FT DOMAIN 374 392
 FT SEQUENCE 482 AA; 34742 MW; 3E789DFC4247E98A CRC64;
 SO
 Query Match 7.7%; Score 97; DB 1; Length 482;
 Best Local Similarity 18.4%; Pred. No. 1.6;
 Matches 54; Conservative 53; Mismatches 89; Indels 98; Gaps 11;
 QY 12 IYQLLEFNPVKTGICRNRNTNNKDYTKLVANLPKDYITL----- 55
 DB 27 IYLDALFHSYLAEDDL-KQLLSINKTELGLPLARLRSDDLISIKOREYPPNSKSVERY 85
 QY 56 ----KYVGMQVLPSCW-ISEMVVQLSDSLTD-----LIDKFSNI----- 91
 DB 86 YYYVYKPAIDAIR--WKVHQVQRLKDDLDKNSPBGWCPICLTFTYQLLEAVQLNF 142
 QY 92 -----SEGLSNYSIDKLNYVDLVECV-----KENSMDLKKSRSP 130
 DB 143 DRTFELCSICDEPLEVDESGKKNKEKDKLNLMDQIPIIDSLKKIDSDISENTEIA 202
 QY 131 ERLTTPPEFFRIFNRSIDAFKDFVASETSCVVSSTLSPEKGRKAKNPDDSSLHMAAM 190
 DB 203 IARLIPQ-----NOSHAA-----TYNKKSGTMRPPDSA----- 234
 QY 191 ALPAFLSLICGFAGALYWKKROPSLTRAVENTIOINEEDNLSMLQEKREFOE 244
 DB 235 PLPNTMGTLGDS-----SRRAGANSQATLTIINTTASDEVAQELQERQAE 283
 RESULT 8
 RAGE MOUSE STANDARD: PRT; 403 AA.
 AC 062151:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 01-MAR-2002 (Rel. 41, last annotation update)
 DE Advanced glycosylation and product-specific receptor precursor
 DE (receptor for advanced glycosylation end products).
 GN AGER OR RAGE.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Luth E.,
 RA Morser J., Zhao L., Schmidt A.M., Scherrenmann J.M., Wautier J.L.;
 RT "Recombinant advanced glycation end product receptor pharmacokinetics
 RT in normal and diabetic rats";
 RL Mol. Pharmacol. 52:54-62(1997).
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
 CC RATE IN DIABETES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC
 CC EMBL: L33412; AAA40040.1; -
 DR MGD: MGI:893592; Ager.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; IG_Like; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 403
 FT DOMAIN 23 341
 FT TRANSMEM 342 362
 FT DOMAIN 363 403
 FT DOMAIN 31 105
 FT DOMAIN 136 213
 FT DOMAIN 251 307
 FT DISULFID 38 98
 FT DISULFID 143 207
 FT DISULFID 258 300
 FT CARBOHYD 25 25
 FT CARBOHYD 80 80
 FT SEQUENCE 403 AA; 42668 MW; 1279796FD1579357 CRC64;
 SO
 Query Match 7.5%; Score 94.5; DB 1; Length 403;
 Best Local Similarity 26.0%; Pred. No. 2.1; Indels 45; Gaps 7;
 Matches 39; Conservative 19; Mismatches 47;
 QY 112 VECYKENSMDLKKSEKPEPRFTPEEPRIFNRSIDAFKDFVASE-TSDCVSSTLS 170
 DB 268 VHWIKDCAPLPL-----APSPVLLPEVGH-----ADEGYSCVAT---H 304
 QY 171 PEKGRANPP-----GDSSLHMAAMALPALFSL-IIGFAFGALYWK 211
 DB 305 PSHGPQESPPVSIKVTETGDEGPAEGSGVSGIGLTALALGIGLVALLGAILMK 364

QY 12 IYIQLLFNPLVKTEG-----ICRRNRYTNMKDVT-----K 42
 || : | ||: | | : |
 Db 53 IYIEKRLAKPLIKKNGKLVETWDEALSPFAEKLKNYNADITFIASGCTNEDNYALK 11

CC	EMBL	L33413	AAA42027.1	-
DR	InterPro	IPR003306	Ig_MHC	
DR	InterPro	IPR003598	Ig_c2	
DR	InterPro	IPR003600	Ig_1like	
DR	Pfam	PF00047	Ig_3	
DR	SMART	SM00410	Ig_1like	1
DR	SMART	PS00408	IGC2	1
DR	PROSITE	PS00290	Ig_MHC	1
DR	Immunoglobulin domain			
DR	Signal	1	22	POTENTIAL.
DR	CHAIN	23	402	POTENTIAL.
DR	DOMAIN	23	341	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR.
DR	TRANSMEM	342	362	EXTRACELLULAR (POTENTIAL).
DR				POTENTIAL.

FT DOMAIN 363 402 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 31 105 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 212 212 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 250 306 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 38 98 POTENTIAL.
 FT DISULFID 143 206 POTENTIAL.
 FT DISULFID 257 299 POTENTIAL.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 402 AA; 42663 MW; 594481BC3A51E94E CRC64;

Query Match 7.2%; Score 91; DB 1; Length 402;
 Best Local Similarity 27.3%; Pred. No. 4;
 Matches 36; Conservative 12; Mismatches 46; Indels 38; Gaps 5;

OY 129 SPEERLFTPEEFFRIFNRSIDAFKDVASSTDCVVSSTLSPEKGNKP----- 180
 DB 279 APSVYLLP-----VGHEDGITYSCVATHPSHGQESPVNIRVTER 321
 OY 181 GD-----SSLHMANALPALFSL-IIGFAFGALYKKRPSL--TRAVENIOINE 227
 DB 322 GDEGQAGSVYDSSGLGTALALGILGIALALLIGAILMKRKPRLERKAPESODEE 381
 OY 228 EDNEISMLOEKE 239
 DB 382 ERAELNOSSEAE 393

RESULT 11
 SCAI_RICE STANDARD; PRT; 981 AA.
 AC 09A37; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
 DE (Protein PS 120) (Fragment).
 CN SCAI OR D.
 OS Rickettsia felis (Rickettsia azadi).
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=42862;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sekyova Z., Roux V., Raoult D.;
 RT "Phylogenetic analysis of Rickettsia spp. by comparing the sequence of
 gene D coding for an intracytoplasmic protein.";
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
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 CC
 CC EMBL: AF196973; AAK1304.1; -.
 DR Antigen.
 KW NON_TER 1
 FT NON_TER 981
 SQ SEQUENCE 981 AA; 107514 MW; 7F18F421E2C262E1 CRC64;

Query Match 7.2%; Score 91; DB 1; Length 981;
 Best Local Similarity 25.1%; Pred. No. 12;
 Matches 48; Conservative 24; Mismatches 59; Indels 60; Gaps 10;
 OY 19 FNPLVTEGICRNRVTNNVKD-----VTKLIVANLPKDYMITLKYVPGM-DV 63
 DB 628 FNITAKTEAI--QNTTKYLDSPKRAIGETLESTITKVVASPLNGQKAIIVAGMGA 685

OY 64 LPSH-----CWISMVYQLSDSLFDLDR-----FSNISEGLSNYSI----- 100
 DB 666 IASHSTYMAPTEKISTSTSEVEKGVASTITDLEDKLMTKGLVGEIGANPEISETKA 745
 OY 101 ----IDKLIVNYVD--LVECKE-----NSSKDIK-SEKSPERLFTPEEFFRI 144
 DB 746 VSRGIDKSTALPREDQALKDANEAALDRETONLTEGILKRONLGPCKPR-----DDIYNKA 801
 OY 145 NRSIDAFKDFV 155
 DB 802 QDVADALKNVI 812

RESULT 12
 POL_RTBVP STANDARD; PRT; 1675 AA.
 AC P27502; P27528; 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Polypeptide (p194 protein) [Contains: Coat protein; Protease
 (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Ribonuclease H
 (EC 3.1.26.4)].
 OS Rice tungro bacilliform virus (isolate Philippines) (RTBV).
 OC Viruses; Retroid viruses.
 OX NCBI_TaxID=10655;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91252204; PubMed=2041739;
 RA Hay J.M., Jones M.C., Blakebrough M.L., Dasgupta I., Davies J.W.,
 RA Hull R.;
 RT "An analysis of the sequence of an infectious clone of rice tungro
 bacilliform virus, a plant pararetrovirus.";
 RL Nucleic Acids Res. 19:2615-2621(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 503-526.
 RX MEDLINE=92024093; PubMed=1926781;
 RA Ou R.D., Bhattacharya M., Laco G.S., de Kochko A., Rao B.L.S.,
 RA Kanleska M.B., Elmer J.S., Rochester D.E., Smith C.E.,
 RA Beachy R.N.;
 RT "Characterization of the genome of rice tungro bacilliform virus:
 comparison with Commelina yellow mottle virus and caulimoviruses.";
 RL Virology 185:354-364(1991).
 CC -1- SIMILARITY: WITH COMMELINA YELLOW MOTTLE VIRUS POLYPROTEIN, AND
 WITH CAULIMOVIRUSES ORF V.
 CC -1- SIMILARITY: WITH RETROVIRAL POL/GAG POLYPROTEINS.
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 CC
 CC EMBL: X57924; CAA0097.1; -.
 DR EMBL: M65026; AAB03094.1; -.
 DR PIR: C40785; C40785.
 DR MEROPS: A03.002; -.
 DR InterPro: IPR001995; Asp. prot. retrov.
 DR InterPro: IPR001969; Asp. protease.
 DR InterPro: IPR000477; RTase.
 DR InterPro: IPR001878; ZnF_CCHC.
 DR Pfam: PF00077; rvp; 1.
 DR Pfam: PF00078; rvt; 1.
 DR Pfam: PF00098; zf-CCHC; 1.
 DR SMART: SM00343; ZnF_C2HC; 1.
 DR PROSITE: PS00141; ASP_PROTEASE; 1.
 DR Polyprotein: RNA-directed DNA polymerase; Hydrolyase;
 KW Aspartyl protease; transferase; Nucleotidyltransferase; Coat protein;
 Endonuclease; Zinc-finger.

FT CHAIN 503 ? 33 KDA COAT PROTEIN.
 FT ZN_FING 772 789 POTENTIAL.
 FT ACT_SITE 987 987 PROTEASE (BY SIMILARITY).
 FT CONFLICT 1292 1292 D->E (IN REF. 2).
 FT CONFLICT 1630 1630 Y->H (IN REF. 2).
 FT CONFLICT 1635 1635 S->P (IN REF. 2).
 SQ SEQUENCE 1675 AA; 194081 MW; B24D7181463E466F CRC64;

Query Match 7.2%; Score 90.5; DB 1; Length 1675;
 Best Local Similarity 25.6%; Pred. No. 25;

Matches 56; Conservative 35; Mismatches 87; Indels 41; Gaps 12;

QY 35 NNKDVTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMYVQSDSLTDLDFKS-----N 90
 DB 1362 NKKVEGCVLSK--KSKMFLKEVEYLG-----EIKGKISLOPHIVDIKFKDKKKLN 1414
 QY 91 ISEGISNT-SIIDKLVNIYVDLVECVKENSCKDKSKSPKSEPLFTPEEFPRIF--NRS 147
 DB 1415 TLKGLQATLGLNARGYIKDKSLV-----GPLYKKTGKNGQ-RIFNKEDMNIIFKIERE 1469
 QY 148 IDAFKDVVASETSDCVVSTLSPEKGRKKNPGDSSLHMAAAL--PALFS-----LI 200
 DB 1470 VSKIPLEPRKET-DYIIETDASEEG-----WGAVLVCKPKDKYSGKTEKIA 1516
 QY 201 GAFAFALYWKRRQPSLTRAVENTIQINEDNEISMLOEKE 239
 DB 1517 GYASGNFGEKKTWTSLDYEIE--AINELANKFOIYLDKD 1553

RESULT 13

PK1_NPVHZ STANDARD; PRT; 267 AA.

AC P41719; 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Serine/threonine-protein kinase 1 (EC 2.7.1.1-).
 GN PK1 OR PK-1.
 OS Heliothis zea nuclear polyhedrosis virus (HsNPV) (Helicoverpa zea single nucleocapsid nuclear polyhedrosis virus)
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 OX NCBI_Taxid=28290;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ELKAR;
 RA Tribe D.; Bulach D.M., Goodge K., Robertson A.P.S., Wu T., Lee H., McAdams A., Cowan P.J.;
 RX MEDLINE=97321796; PubMed=9178498;
 RA Le T.H., Wu T., Robertson A.P.S., Bulach D.M., Cowan P.J., Goodge K., Tribe D.;
 RT "Genetically variable triplet repeats in a RING-finger ORF of Helicoverpa species baculoviruses";
 RL Virus Res. 49:67-77(1997).
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES.
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 CC -----
 CC EMBL, L36721; AAA50302.1; -;
 DR EMBL, U67264; AAB54091.1; -;
 DR HSP; P05132; ICRP.

DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase.1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP, FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST, 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM, 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 18 266
 FT NP_BIND 24 32
 FT BINDING 47 47
 FT ACT_SITE 134 134
 SQ SEQUENCE 267 AA; 31531 MW; DIFB332CEC16AD53 CRC64;

Query Match 7.1%; Score 90; DB 1; Length 267;
 Best Local Similarity 23.1%; Pred. No. 2.9;

Matches 50; Conservative 34; Mismatches 78; Indels 54; Gaps 11;

QY 37 VKDYTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMYVQSDSLTDLDFKSNISG 94
 DB 54 VTELEPLVHQMKDNRYFIKLY--SLTTLKSQILILDYVA--GDDLFPFLKKKKVSEA 109
 QY 95 LSNTSIIDKLVNIYVDLVECVKENSCKDKSKSPKSEPLFTPEEF-----RIFNS 147
 DB 110 -ETRSIVGQLFEALNAL-----HSYKTIINDKLENLVYRRKQIYLDYGLCKIVNTS 162
 QY 148 I-DAFKDVVASETSDCVVSTLSPEKGRKKNPGDSSLHMAAALPALFSLTIGFAG 205
 DB 163 SCRDTKEY-----MSPEKLRQN--YDVHVMWALGI-LTYELLIGH--- 202
 QY 206 ALYKKRQPSLTRAVENTIQINEDNEISMLOEKERE 241
 DB 203 -----HPKHSNDNEEDFDLDVLOQRQK 226

RESULT 14

RMUC_CHLPN STANDARD; PRT; 411 AA.

AC O92657; 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE DNA recombination protein rmuc homolog.
 GN RMUC OR CPN0982 OR CP0874.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=83358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CM1029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gail S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Ullrich T., Berry K., Bass S., Liner K., Weldon J., Khouri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae Ar39";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;

```

RT      "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT      from Japan and CH1029 from USA."
RL      Nucleic Acids Res. 28:2311-2314(2000).
CC      -1- FUNCTION: Involved in DNA recombination (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE RMOC FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AE001678; AAD19119.1; -.
DR      EMBL: AE002246; AAP38663.1; -.
DR      EMBL: AF002548; BAA99189.1; -.
DR      TIGR: CP0874; -.
DR      InterPro: IPR003798; DUF195.
DR      Pfam: PF02646; DUF195.1.
KW      DNA recombination; Coiled coil; Complete proteome.
FT      DOMAIN 26 64 COILED COIL (POTENTIAL).
FT      DOMAIN 123 143 COILED COIL (POTENTIAL).
SQ      SEQUENCE 411 AA; 47020 MW; 976E6EC1708581E CRC64;

Query Match
Best Local Similarity 7.1%; Score 90; DB 1; Length 411;
Matches 45; Conservative 33; Mismatches 56; Indels 44; Gaps 9;

QY 71 SEMVVOUSDSTLDLDFKSNISEGLSNYSITIDKLVNIYVDLVEGVKNSKDLKKSP-RS 129
DB 195 ADIIRLPQDRCLITDKAPISDSYFVEIDK-GDLVDIKETIKETIKLTKSKTWEKPHQS 253
QY 130 PE-PLFTPEPEFFRIFNKSIDAFKDFVVASSETSDCVSVSTLSPEKGRKKNPPGDSILHMA 188
DB 254 PEYIILFPGF--SLFNDAIRLAPELMEIGASSNVIISSPLT----- 293
QY 189 AMALPAIFSLIIGFAGALYKKRQPSLTRAVENIQINEEDNEISML-QEKEREFOEV 245
DB 294 ---LIALIKTI-----AYMKQ-----ENIQ-KQIQEVSLLGKELHRLQV 331

RESULT 15
RRPL_BUNWV STANDARD; PRT: 2238 AA.
AC P20470;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (L protein).
GN L.
OS Bunyavera virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Bunyavirus.
OX NCBI_TaxID=11573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90085791; PubMed=2596023;
RA Elliott R.M.;
RT "Nucleotide sequence analysis of the large (L) genomic RNA segment of
RT Bunyavera virus, the prototype of the family Bunyaviridae.";
RL Virology 173:426-436(1989).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----

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DR      EMBL: X14383; CA32553.1; -.
DR      PIR: A33744; RRYUBY.
DR      Transferase: Nucleotidyltransferase; RNA-directed RNA polymerase.
SQ      SEQUENCE 2238 AA; 258668 MW; 1ED00AB156BAC8DA CRC64;

Query Match
Best Local Similarity 7.1%; Score 89; DB 1; Length 2238;
Matches 70; Conservative 41; Mismatches 108; Indels 108; Gaps 17;

QY 2 KKTQWILTCIYLQDLLFNP-----LVKTEG-----ICRNRYTN 35
DB 1064 EKTRILYMCNVMQKLLIPDDLJANILDDQRPYNDDLIEMTGLNRYVQIKRMVLOG 1123
QY 36 NVKDYTKLVANLPKDYMTTLKYV--PGNDVLPSCWISSEWVVOUSDSTLDLDFKSNISE 93
DB 1124 NFNYISYVHSCA--MLVYKDILKECKMLDGDCLNSM-VHSDDNQTSL-----AIIQN 1175
QY 94 GLSNYSITIDKLVNIYVDLVEGVKNSKDLKKSPSPRLPTPEFFRIFN--RSIDA 150
DB 1176 KVSDDIVQYANPTESV--CLTFGCGANMKKTYIT-----HTCKEFVSLFNHGEPLSV 1228
QY 151 FKDFVVASSETSDCV-----VSTLSPEKGRKAN--PGDSSLHMAAMA----- 191
DB 1229 FGRFLIPS-VGDCAYIGPYEDLASRLSAQOSLKRHCPP--SLVWLAISSCHWITFTTY 1284
QY 192 -----LPAIFSLIIGFAGALYV-----KKRQPS 215
DB 1285 NMLDDQINAPQOHLFPNNRKEIPVELNGYLNAPFLIIMLVGLGNNLFLNLIKRVLP- 1343
QY 216 LTRAVENIQIN--EEDNEISMLQEKER 240
DB 1344 LDKQKETIQSOCLHLCSNIDKLTSESK 1370

Search completed: August 18, 2002, 13:02:08
Job time: 53 sec

```

Sun Aug 18 14:09:06 2002

us-09-604-325a-63.rsp

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 13:06:05 ; Search time 114.11 Seconds

(Without alignments)
371.429 Million cell updates/sec

Title: US-09-604-325A-63

Perfect score: 1262

Sequence: 1 MKKTQTWILTCIYLQLLFNN.....NEDNEISMLOEKEREPQEV 245

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMEL19:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1249	99.0	245	4	Q90K7
2	1051.5	83.3	274	6	P79169
3	1031	81.7	245	11	Q92287
4	1022.5	81.0	260	6	Q95MNS
5	1021.5	80.9	274	6	Q95M19
6	1018.5	80.7	274	6	Q28132
7	1014.5	80.4	274	6	Q95N18
8	1009	80.0	245	11	Q64222
9	992	78.6	273	11	Q90M24
10	991	78.5	273	11	Q9QW24
11	991	78.5	273	11	Q921N5
12	990.5	78.5	267	6	P79368
13	990	78.4	273	11	P97332
14	988.5	78.3	261	6	Q95MD2
15	951.5	75.4	256	6	Q62765
16	715	56.7	208	11	Q64384

17	605	47.9	253	13	Q90315	Q90315	coturnix co
18	583	46.2	287	13	Q90314	Q90314	coturnix co
19	509	40.3	123	11	Q61854	Q61854	mus musculus
20	339	26.9	271	13	Q9YGP2	Q9YGP2	ambystoma m
21	282	22.3	54	4	Q16487	Q16487	homo sapien
22	265.5	21.0	96	6	Q95MG8	Q95MG8	equus caball
23	223.5	17.7	47	6	Q95MG7	Q95MG7	equus caball
24	136	10.8	36	6	Q9T074	Q9T074	equus caball
25	109	8.6	937	10	Q9M1A4	Q9M1A4	bos taurus
26	102.5	8.1	1498	3	Q9P884	Q9P884	arabidopsis
27	102.5	8.1	1498	3	Q9P884	Q9P884	arabidopsis
28	102.5	8.1	1498	3	Q9P884	Q9P884	arabidopsis
29	102.5	8.1	1498	3	Q9P884	Q9P884	arabidopsis
30	100.5	8.0	1501	3	Q96VY9	Q96VY9	emeritella
31	99	7.8	539	12	Q91H18	Q91H18	botrytis ci
32	97.5	7.7	402	11	Q35444	Q35444	discula des
33	97	7.7	1447	16	Q9P0J8	Q9P0J8	ureaplasma
34	94.5	7.5	1515	3	Q96VY4	Q96VY4	emeritella
35	93.5	7.4	576	11	Q62970	Q62970	rattus norv
36	93.5	7.4	647	16	Q98PP9	Q98PP9	mycoplasma
37	93.5	7.4	3227	3	Q13834	Q13834	schistosom
38	93	7.4	1298	10	Q9ISA4	Q9ISA4	arabidopsis
39	93	7.4	1962	10	Q9R162	Q9R162	arabidopsis
40	92.5	7.3	512	16	Q9CGA7	Q9CGA7	lactococcus
41	92.5	7.3	534	5	Q21299	Q21299	caenorhabdi
42	92	7.3	420	16	Q96QW8	Q96QW8	mycoplasma
43	92	7.3	821	16	Q92E65	Q92E65	listeria in
44	91.5	7.3	1993	5	P90670	P90670	aplysia cal
45	91	7.2	317	5	Q9VY22	Q9VY22	dirosophila

ALIGNMENTS

RESULT 1
ID Q90K7 PRELIMINARY: PRT: 245 AA.
AC Q90K7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STEM CELL FACTOR (STEM CELL FACTOR ISOFORM 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99160429; PubMed-10049787;
RA Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.;
RT "Parathyroid hormone-regulated production of stem cell factor in human
RT osteoblasts and osteoblast-like cells."
RN Biochem. Biophys. Res. Commun. 255:778-784(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Han C., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF119835; AAD22048.1; -;
DR EMBL; AF400437; AAK92486.1; -;
DR InterPro; IPR003452; SCF.
DR Pfam; PF02404; SCF; 1.
SQ SEQUENCE 245 AA; 27903 MM; FF87983163A3C36 CRC64;

Query Match 99.0%; Score 1249; DB 4; Length 245;
Best Local Similarity 98.8%; Pred. No. 1.2e-98;

Matches 242; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKTQTWILTCIYLQLLFNNPVTGEGICRRVNNKDYKLVANPKRYMTITVYRG 60
DB 1 MKKTQTWILTCIYLQLLFNNPVTGEGICRRVNNKDYKLVANPKRYMTITVYRG 60
QY 61 MDVLSHCWISLWVQSLDSTLDLDFKFSNISSELSVSIIDKLVIVDDLVCEVRENS 120

Query Match	83.3%	Score 1051.5	DB 6	Length 274
Best Local Similarity	76.6%	Pred. No. 9.4e-82		
Matches	210	Conservative	17	Mismatches 18; Indels 29; Gaps 2
QY	1	MKKTQWILTCIYLQLLLENPVLTKEGICRNRVYNNVKDVTKIYANLPKDYMITLKYVG	60	
Db	1	MKKTQWIVTGCYIQLLENPVLTKEGICRNRVYNNVKDVTKIYANLPKDYMITLKYVG	60	
QY	61	MDVLPCHCMTSEMYVOLSDSTDLDKFNSISGSLNSYITDKLVNIYDVLVCYCKENS	120	
Db	61	MDVLPCHCMTSEMYVOLSDSTDLDKFNSISGSLNSYITDKLVNIYDVLVCYCKENS	120	
QY	121	KDLKSEFKSBEPRLPFPEEFERIFENSIDAFKDF-VVASETSDCVVSTLSPKSG----	174	
Db	121	ENVKSSKSSEPRLPFPEEFERIFENSIDAFKDFLEMAVASKTSCEVYVSTLSPKDSRSVY	180	
QY	175	-----KANNPDDSSLHMAAMLPLSLTIGFAFGALYWK	211	
Db	181	TKPFMLPVAASLRDSSSNRKANIPLEDSSIQWVMAALPACFSVLIGFAFGALYWK	240	
QY	212	ROPSLTRAVENTIQINEEDNEISMLOEKEREFQY	245	
Db	241	KQPNLRTVENIQINEEDNEISMLOEKEREFQY	274	
RESULT	3			
ID	Q9Z2E7	PRELIMINARY;	PRT;	245 AA.
AC	Q9Z2E7;			
DT	01-MAY-1999 (TEMBLrel. 10, Created)			
DT	01-MAY-1999 (TEMBLrel. 10, Last sequence update)			

Query Match	81.7%;	Score 1031;	DB 11;	Length 245;
Best Local Similarity	80.8%;	Pred. No. 4.5e-80;		
Matches 198;	Conservative 18;	Mismatches 29;	Indels 0;	Gaps 0;

Query Match	Similarity	81.0%	Score 1022.5	DB 6	Length 260
Best Local	Similarity	80.7%	Pred. No. 2.6e-79		
Matches	Conservative	22	Mismatches	24	Indels
					Gaps
QY	1	MKTQPTMILLCITQILLLFNPLVETSGICGNRTYNNKDYKTVLVANLPKDYMITLKEVGG	60		
Db	1	MKTQPTMILLCITQILLLFNPLVETSGICGNRTYTDVKDYKTVLVANLPKDYKITALVYVGG	60		
QY	61	MDVLPISHCWISENVQVSDSLTDLDDKFNISISGSLSYSTIDKLVTNIVVDLVCEKVENNS	120		

RESULT	6	
Q28132	PRELIMINARY;	PRT; 274 AA.
Q28132		
Q28133;		
PT 01-NOV-1996	(TREMBLrel. 01, Created)	
PT 01-NOV-1996	(TREMBLrel. 01, Last sequence update)	

	RESULT	7	
D	95NM18	PRELIMINARY;	PRT; 274 AA.
T	095N18:		
C	01-DEC-2001 (TEMBLrel. 19,		
T	01-DEC-2001 (TEMBLrel. 19,		
T	01-DEC-2001 (TEMBLrel. 19,		
E	STEM CELL FACTOR LONG ISOFORM.		
S	Mustela vison (American mink).		
S	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;		
C	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae		
X	NCBI_TaxID=9667;		
N	[1]		
P	SEQUENCE FROM N.A.		
A	Bennett R.D., Murphy B.D.;		
T	"Stem Cell Factor long form."		
L	Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.		
L	EMBL; AY013712; AAG37434.1; -		

SEQUENCE 274 AA; 31034 MW; 5AC1619014AF5E72 CRC64;

Query Match 80.4%; Score 1014.5; DB 6; Length 274;
Best Local Similarity 73.7%; Pred. No. 1.3e-78;
Matches 202; Conservative 20; Mismatches 23; Indels 29; Gaps 2;

QY 1 MKKTQWITTCIYIQLLEFNPVLTKEGICRNRYNNVADYKLVANLPKDYMTLTKVPG 60
DB 1 MKKTQWITTCIYIQLLEFNPVLTKEGICRNRYNNVADYKLVANLPKDYMTLTKVPG 60
QY 61 MDVLPSCWISBMVYVQSDSLTDLDFKFSNISEGINSYIIDKLVNYVDLVECVKENS 120
DB 61 MDVLPSCWISBMVYVQSDSLTDLDFKFSNISEGINSYIIDKLVNYVDLVECVKENS 120
QY 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDF-VVASSETSDCVSSTLSPEKG----- 174
DB 121 ENYKSPKPEPRFTPEEFRIFNRSIDALKDLETVAKSTSECVLSTLSPEKDSRVSV 180
QY 175 -----KAKNPPGDSLHMAALPALFSLIIGFAGALYWK 211
DB 181 TKPFMLPVVAASSLRNDSSSNRKAANPLGDSNLCQWAMALPAFFSLVIGFAGALYWK 240
QY 212 RQPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
DB 241 KQPNLTRTAENIOINEDNEISMLOEKEREFOEV 274

RESULT 8
Q64222
ID 064222 PRELIMINARY: PRT: 245 AA.
AC 064222;
DT 01-NOV-1996 (Tremblrel. 01, Created)
RT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
C-Kit LIGAND TRUNCATED TRANSMEMBRANE FORM KL-2.
GN SL/STBEL.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92330001; PubMed=1378327;
RA Huang E.J., Nocka K.H., Buck J., Besmer P.;
RT "Differential expression and processing of two cell associated forms
of the kit-ligand: KL-1 and KL-2."
RL Mol. Biol. Cell 3:349-362(1992).
DR EMBL: S40534; AAB2555.2; -;
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
KW Transmembrane.
SQ SEQUENCE 245 AA; 27541 MW; 7816113BAF0E23B CRC64;

Query Match 80.0%; Score 1009; DB 11; Length 245;
Best Local Similarity 80.4%; Pred. No. 3.4e-78;
Matches 197; Conservative 19; Mismatches 29; Indels 0; Gaps 0;

QY 1 MKKTQWITTCIYIQLLEFNPVLTKEGICRNRYNNVADYKLVANLPKDYMTLTKVPG 60
DB 1 MKKTQWITTCIYIQLLEFNPVLTKEGICRNRYNNVADYKLVANLPKDYMTLTKVPG 60
QY 61 MDVLPSCWISBMVYVQSDSLTDLDFKFSNISEGINSYIIDKLVNYVDLVECVKENS 120
DB 61 MDVLPSCWISBMVYVQSDSLTDLDFKFSNISEGINSYIIDKLVNYVDLVECVKENS 120
QY 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKGAKNP 180
DB 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKGAKNP 180
QY 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKGAKNP 180
DB 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKGAKNP 180
QY 181 GSSSLHMAALPALFSLIIGFAGALYWKROPSTRAVENTIOINEDNEISMLOEKER 240
DB 181 GSSSLHMAALPALFSLIIGFAGALYWKROPSTRAVENTIOINEDNEISMLOEKER 240

DB 181 EDSGIQTALAPALISLVIGFAGALYWKKOSLTRAVENTIOINEDNEISMLOEKER 240

QY 241 EFOEV 245
DB 241 EFOEV 245

RESULT 9
Q9QWZ4
ID 09QWZ4 PRELIMINARY: PRT: 273 AA.
AC 09QWZ4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
RT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE STEM CELL FACTOR KL-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Teramoto T., Nagashima M., Thorgeirsson S.S.;
RT "Rat-SCF-KL-1."
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF071204; AAD02827.1; -;
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1.
KW
SQ SEQUENCE 273 AA; 30712 MW; C0F56527DC93FD27 CRC64;

Query Match 78.6%; Score 992; DB 11; Length 273;
Best Local Similarity 71.8%; Pred. No. 1.1e-76;
Matches 196; Conservative 18; Mismatches 31; Indels 28; Gaps 1;

QY 1 MKKTQWITTCIYIQLLEFNPVLTKEGICRNRYNNVADYKLVANLPKDYMTLTKVPG 60
DB 1 MKKTQWITTCIYIQLLEFNPVLTKEGICRNRYNNVADYKLVANLPKDYMTLTKVPG 60
QY 61 MDVLPSCWISBMVYVQSDSLTDLDFKFSNISEGINSYIIDKLVNYVDLVECVKENS 120
DB 61 MDVLPSCWISBMVYVQSDSLTDLDFKFSNISEGINSYIIDKLVNYVDLVECVKENS 120
QY 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKG----- 174
DB 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKG----- 174
QY 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKG----- 174
DB 121 KDLKSFSPKPEPRFTPEEFRIFNRSIDAFKDFVVASSETSDCVSSTLSPEKG----- 174
QY 175 -----KAKNPPGDSLHMAALPALFSLIIGFAGALYWK 212
DB 181 KPFMLPVVAASSLRNDSSSNRKAAPDPGLOWTAMALPALISLVIGFAGALYWK 240
QY 213 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 245
DB 241 QPSLTRAVENTIOINEDNEISMLOEKEREFOEV 273

RESULT 10
Q62524
ID 062524 PRELIMINARY: PRT: 273 AA.
AC 062524;
DT 01-NOV-1996 (Tremblrel. 01, Created)
RT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE MAST CELL GROWTH FACTOR.
GN KITL OR MGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ; TISSUE=Brain;
RX MEDLINE=97032534; PubMed=8875893;
KW Graw J., Loester J., Neuhäuser-Klaus A., Pretsch W., Schmitt-John T.;

"Molecular analysis of two new Steel mutations in mice shows a RT transversion or an insertion".
 RT Mamm. Genome 7:843-846(1996).
 DR EMBL: X99322; CA67698.1; -.
 DR MGD: MGI:96974; KIL.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF, 1.
 FT VARIANT 193 193 P -> L.
 FT VARIANT 207 207 S -> A.
 SQ SEQUENCE 273 AA: 30645 MW: B3E9D0B72C734107 CRC64;

Query Match 78.5%; Score 991; DB 11; Length 273;
 Best Local Similarity 72.2%; Pred. No. 1.3e-76;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

QY 1 MKKTQWITTCYIQLLLFPNPLVKTGICRNRVNNKVDYTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITTCYIQLLLFPNPLVKTGICRNRVNNKVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCMISEMAYVOLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCMISEMAYVOLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSFSPPEPRLETPPEFFRIFNRSIDAFKDFVVASETSDCVVSTLSPKSG----- 174
 DB 121 KDLKSFSPPEPRLETPPEFFRIFNRSIDAFKDFVVASETSDCVVSTLSPKSG----- 174
 QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWK 212
 DB 181 KPFMLPVAASSLRNDSSSNRKAASPEDSGLOMTAMALPALISLVIGFAGALYWK 240
 QY 213 QPSLTRAVENTIQINEEDNEISMLOEKERFQEV 245
 DB 241 QSSLTRAVENTIQINEEDNEISMLOEKERFQEV 273

RESULT 11
 ID Q921N5 PRELIMINARY; PRT; 273 AA.
 AC Q921N5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SMITLAR TO KIT LIGAND.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC013322; AAH1322.1; -.
 SQ SEQUENCE 273 AA: 30661 MW: A7FC91E3939320107 CRC64;

Query Match 78.5%; Score 991; DB 11; Length 273;
 Best Local Similarity 72.2%; Pred. No. 1.3e-76;
 Matches 197; Conservative 19; Mismatches 29; Indels 28; Gaps 1;

QY 1 MKKTQWITTCYIQLLLFPNPLVKTGICRNRVNNKVDYTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITTCYIQLLLFPNPLVKTGICRNRVNNKVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCMISEMAYVOLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCMISEMAYVOLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSFSPPEPRLETPPEFFRIFNRSIDAFKDFVVASETSDCVVSTLSPKSG----- 174
 DB 121 KDLKSFSPPEPRLETPPEFFRIFNRSIDAFKDFVVASETSDCVVSTLSPKSG----- 174
 QY 121 KDLKSFSPPEPRLETPPEFFRIFNRSIDAFKDFVVASETSDCVVSTLSPKSG----- 174
 DB 121 KDLKSFSPPEPRLETPPEFFRIFNRSIDAFKDFVVASETSDCVVSTLSPKSG----- 174

QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWK 212
 DB 181 KPFMLPVAASSLRNDSSSNRKAASPEDSGLOMTAMALPALISLVIGFAGALYWK 240
 QY 213 QPSLTRAVENTIQINEEDNEISMLOEKERFQEV 245
 DB 241 QSSLTRAVENTIQINEEDNEISMLOEKERFQEV 273

RESULT 12
 ID P79368 PRELIMINARY; PRT; 267 AA.
 AC P79368; Q28591;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE STEM CELL FACTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN [1]
 RP SEQUENCE OF 8-267 FROM N.A.
 RC TISSUE-OVARIAN FOLLICLE;
 RX MEDLINE-96413880; PubMed-8662240;
 RA Tisdall D.J., Quirke L.D., Galloway S.M.;
 RT "Ovine stem cell factor gene is located within a syntenic group on
 chromosome 3 conserved across mammalian species.";
 RL Mamm. Genome 7:472-473(1996).
 RN [2]
 RP SEQUENCE OF 8-267 FROM N.A.
 RC TISSUE-OVARIAN FOLLICLE;
 RA Tisdall D.J., Quirke L.D.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-202 FROM N.A.
 RA McInnes C.J., Logan M., Falconer V.M., Rawlins P., Huntly J., Haig D.;
 RL Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U89874; AAB49491.1; -.
 DR EMBL: 250743; CAA90620.1; -.
 DR InterPro: IPR003452; SCF.
 DR Pfam: PF02404; SCF, 1.
 FT NON_TER 267
 SQ SEQUENCE 267 AA: 30148 MW: 909D959E4B9EC841 CRC64;

Query Match 78.5%; Score 990.5; DB 6; Length 267;
 Best Local Similarity 74.2%; Pred. No. 1.4e-76;
 Matches 198; Conservative 19; Mismatches 21; Indels 29; Gaps 2;

QY 1 MKKTQWITTCYIQLLLFPNPLVKTGICRNRVNNKVDYTKLVANLPKDYMITLKYPG 60
 DB 1 MKKTQWITTCYIQLLLFPNPLVKTGICRNRVNNKVDYTKLVANLPKDYMITLKYPG 60
 QY 61 MDVLPSCMISEMAYVOLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 DB 61 MDVLPSCMISEMAYVOLSDSLDLDKFSNISSEGLSNYSIIDKLVNIYVDLVECKENSS 120
 QY 121 KDLKSFSPPEPRLETPPEFFRIFNRSIDAFKDFVVASETSDCVVSTLSPKSG----- 174
 DB 121 KDLKSFSPPEPRLETPPEFFRIFNRSIDAFKDFVVASETSDCVVSTLSPKSG----- 174
 QY 175 -----KAKNPPGDSLSHMAAMALPALFSLIIGFAGALYWK 211
 DB 181 KPFMLPVAASSLRNDSSSNRKAASPEDSGLOMTAMALPALISLVIGFAGALYWK 240
 QY 212 QPSLTRAVENTIQINEEDNEISMLOEK 238
 DB 241 KQPNLRTVENRQINEEDNEISMLOEK 267

RESULT 13

P97332
ID P97332 PRELIMINARY: PRT: 273 AA.
AC P97332:
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MAST CELL GROWTH FACTOR.
KITL OR MGF S1-3NEU.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=102/E1X3H/E1; Pubmed=9360640;
RX MEDLINE=98025115; PubMed=9360640;
RA Graw J., Neuhäuser-Klaus, Pletsch;
RT "Detection of a point mutation (A to G) in exon 5 of the murine Mgf
gene defines a novel allele at the Steel locus with a weak
phenotype.";
RL Mutat. Res. Genomics 382:75-78(1997).
DR EMBL: Y10287; CAAT1329.1; -
DR MGD: MGI:96974; Kitl.
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1
FT VARIANT 193 193 P -> L.
FT VARIANT 207 207 S -> A.
SQ SEQUENCE 273 AA; 30618 MW; BC36F17A2C6F90C3 CRC64;

Query Match 78.4%; Score 990; DB 11; Length 273;
Best Local Similarity 72.2%; Pred. No. 1.6e-76;
Matches 197; Conservative 18; Mismatches 30; Indels 28; Gaps 1;

QY 1 MKKTQWTLCTIYQLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPG 60
DB 1 MKKTQWTLCTIYQLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLNVA 60
QY 61 MDVLPSCWISSEMYVOLSSTLDLDFKSNISSEGLSNYSIIDKLVNIVDDLVECVKNS 120
DB 61 MDVLPSCWISSEMYVOLSSTLDLDFKSNISSEGLSNYSIIDKLVNIVDDLVECVKNS 120
QY 121 KDLKSKFSPPEPLFTPEEFIRNRSIDAKDFVVASETSDCVVSTLSPEKG----- 174
DB 121 KDLKSKFSPPEPLFTPEEFIRNRSIDAKDFVVASETSDCVVSTLSPEKG----- 174
QY 121 KSIKESPKRPETRSFTPEEFISFNRSIDAKDFVVASETSDCVVSTLSPEKSRVSVT 180
DB 121 KSIKESPKRPETRSFTPEEFISFNRSIDAKDFVVASETSDCVVSTLSPEKSRVSVT 180
QY 175 -----KAKNPPGDSLSHMAAMALPALSLIIGFAGALYWKRR 212
DB 181 KPFMLPYVAASSPRNDSSSNRKAASPEDSGLQMTAMALPALSLIIGFAGALYWKRR 240
QY 213 OSLTRAVENTIOINEEDNEISMLOEKEREPOEV 245
DB 241 OSLTRAVENTIOINEEDNEISMLOEKEREPOEV 273

RESULT 14
Q95MD2 PRELIMINARY: PRT: 261 AA.

ID Q95MD2
AC Q95MD2:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MAST CELL GROWTH FACTOR (FRAGMENT).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
OX [1]
RN SEQUENCE FROM N.A.
RP Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Bailey E.;
RT "Equus caballus mast cell growth factor (MGF).";
RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF401625; AAK94474.1; -

FT NON_TER 1 1
FT NON_TER 261 261
SQ SEQUENCE 261 AA; 29526 MW; 16A3062105346EAB CRC64;

Query Match 78.3%; Score 988.5; DB 6; Length 261;
Best Local Similarity 75.5%; Pred. No. 2.1e-76;
Matches 197; Conservative 19; Mismatches 16; Indels 29; Gaps 2;

QY 4 TQTWLCTIYQLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPGMDV 63
DB 1 TQTWLCTIYQLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPGMDV 60
QY 64 LPSHCWISSEMYVOLSSTLDLDFKSNISSEGLSNYSIIDKLVNIVDDLVECVKNSKDL 123
DB 64 LPSHCWISSEMYVOLSSTLDLDFKSNISSEGLSNYSIIDKLVNIVDDLVECVKNSSENV 120
QY 124 KSKFSKPEPLFTPEEFIRNRSIDAKDF-VVASETSDCVVSTLSPEKG----- 174
DB 121 KSKFSKPEPLFTPEEFIRNRSIDAKDF-VVASETSDCVVSTLSPEKDSRVSTKP 180
QY 175 -----KAKNPPGDSLSHMAAMALPALSLIIGFAGALYWKRR 214
DB 181 FMLPPVAASSLNDSSSNRKAASFTGDSNLQAMAMALPAFFSLVIGFAGALYWKRR 240
QY 215 SLTRAVENTIOINEEDNEISM 235
DB 241 NLTRAVENTIOINEEDNEISM 261

RESULT 15
Q62765 PRELIMINARY: PRT: 256 AA.
ID Q62765
AC Q62765:
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE STEM CELL FACTOR HOMOLOG (FRAGMENT).
GN SCF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=SKIN.
RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
RT "An Equine sequence homologous to stem cell factor (KIT-ligand).";
RT Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF053498; AAC97076.1; -
DR InterPro: IPR003452; SCF.
DR Pfam: PF02404; SCF; 1
FT NON_TER 1 1
FT NON_TER 256 256
SQ SEQUENCE 256 AA; 28933 MW; 9E4876CAEC7B55FF CRC64;

Query Match 75.4%; Score 951.5; DB 6; Length 256;
Best Local Similarity 75.0%; Pred. No. 2.8e-73;
Matches 192; Conservative 18; Mismatches 17; Indels 29; Gaps 2;

QY 12 IYQLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPGMDVLPSCWIS 71
DB 1 IYQLLFNPLVTEGICRNRVTNNKDYTKLVANLPKQYMTTLKYPGMDVLPSCWIS 60
QY 72 EMVOLSSTLDLDFKSNISSEGLSNYSIIDKLVNIVDDLVECVKNSKDLKSKFSPE 131
DB 61 EMVOLSSTLDLDFKSNISSEGLSNYSIIDKLVNIVDDLVECVKNSSENVKSKFSPE 120
QY 132 PLFTPEEFIRNRSIDAKDF-VVASETSDCVVSTLSPEKG----- 174
DB 121 PLFTPEEFIRNRSIDAKDF-VVASETSDCVVSTLSPEKDSRVSTKPMPPLPVAA 180

QY 175 -----KAKNPGDSSLIHWAAALPALFSLITIGFAGALYWKROPSLTRAVEN 222
Db 181 SSLRNDSSSSNRKASFTGDSNLOPAAALPAFFSLVIGFAFAGALYWKROPNLTRAVEN 240
QY 223 IQINEDNEISMLQEK 238
Db 241 IQINEDNEISMLQEK 256

Search completed: August 18, 2002, 13:06:06
Job time: 291 sec

